

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 12, 2004, 11:11:35 ; Search time 21 Seconds
(without alignments)
3041.484 Million cell updates/sec

Title: US-10-087-217A-8

Perfect score: 3475

Sequence: 1 MMTKXNGVKSSPANNHH.....NHEDDVLSDGINTPTAAE 664

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3449	99.3	664	2 S11517	cyclic nucleotide-
2	3231.5	93.0	732	2 S35891	cyclic nucleotide-
3	3204.5	92.2	663	2 S11521	cAMP-gated channel
4	2219.5	63.9	735	2 I50630	alpha subunit of c
5	2140	61.6	706	2 A55251	cyclic nucleotide-
6	2131	61.3	682	1 JH0560	cyclic nucleotide-
7	2126.5	61.2	695	2 S74179	cyclic nucleotide-
8	2067	59.5	645	2 I50680	alpha subunit of r
9	2044	58.8	690	1 S07103	cAMP-gated ion cha
10	2035	58.6	686	1 A44842	cAMP-gated ion cha
11	2030	58.4	630	2 A42161	cAMP-gated cation
12	2017.5	58.1	691	2 JC6509	rod cyclic nucleot
13	1995.5	57.4	688	2 B42161	cAMP-gated cation
14	1518	43.7	575	2 I59327	olfactory cyclic n
15	1487	42.8	665	2 S52072	DmCNGC protein - f
16	1337	38.5	772	2 S28292	hypothetical prote
17	1323	38.1	261	2 I78559	cyclic nucleotide-
18	1160	33.4	261	2 I78560	cyclic nucleotide-
19	866.5	24.9	673	2 T20936	hypothetical prote
20	835	24.0	800	2 T19627	hypothetical prote
21	831	23.9	644	2 T33125	hypothetical prote
22	778	22.4	909	2 S32538	cAMP-gated cation
23	767.5	22.1	611	2 T20935	hypothetical prote
24	596.5	17.2	191	2 S74158	cAMP-gated cation
25	595.5	17.1	189	2 S74159	cAMP-gated cation
26	557.5	16.0	767	2 T21969	hypothetical prote
27	424.5	12.2	962	2 I53197	potassium channel
28	417	12.0	989	2 I48912	potassium channel
29	413	11.9	1102	2 T17367	potassium channel

30	407.5	11.7	1284	2 T13168	probable potassium
31	404.5	11.6	1174	2 A40853	potassium channel
32	395	11.4	1087	2 T31100	probable potassium
33	394	11.3	1159	2 I38465	hypothetical prote
34	382.5	11.0	514	2 T19579	probable potassium
35	380.5	10.9	1017	2 T31354	potassium channel
36	377.5	10.9	688	2 S55349	cyclic nucleotide-
37	376	10.8	716	2 T51354	potassium channel
38	359.5	10.3	662	2 T04461	potassium channel
39	353.5	10.2	934	2 T42394	probable potassium
40	350.5	10.1	845	2 T07052	potassium channel
41	347	10.0	828	2 T52046	probable calmoduli
42	345	9.9	702	2 T04424	hypothetical prote
43	341	9.8	738	2 E85294	cyclic nucleotide
44	337	9.7	698	2 T10541	potassium channel
45	336	9.7	787	2 S68699	potassium channel

ALIGNMENTS

RESULT 1

S11517

cyclic nucleotide-activated channel protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999

C:Accession: S11517

R:Dhalan, R.S.; Yau, K.W.; Schrader, K.A.; Reed, R.R.

Nature 347, 184-187, 1990

A:Title: Primary structure and functional expression of a cyclic nucleotide-activated (

A:Reference number: S11517; MUID:90370115; PMID:1697649

A:Accession: S11517

A:Molecule type: mRNA

A:Residues: 1-664 >DHA>

A:Cross-references: GB:X55519; NID:G56791; PID:CAA39135.1; PID:G56792

C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide

C:Keywords: Transmembrane protein

F:456-580/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP:

Query Match 99.3%; Score 3449; DB 2; Length 664;

Best Local Similarity 99.5%; Pred. No. 7.1e-235;

Matches 661; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	MMTEKXNGVKSSPANNHHPPPSIKANGKDDHRAGSRPQSVAAADDDTSPQLRLAEMDT	60
DB	1	MMTEKXNGVKSSPANNHHPPPSIKANGKDDHRAGSRPQSVAAADDDTSPQLRLAEMDT	60
QY	61	PRRGGGFQRIVRLVGIVRDWANKNPREBEPDPSFLERPRGPELOTVTTHQGDGKGKD	120
DB	61	PRRGGGFQRIVRLVGIVRDWANKNPREBEPDPSFLERPRGPELOTVTTHQGDGKGKD	120
QY	121	GEKGTKKKFELFVLDPAQDWYRMLFVIAMPVLYNKKLIVARACSDIQRNFFVVLVL	180
DB	121	GEKGTKKKFELFVLDPAQDWYRMLFVIAMPVLYNKKLIVARACSDIQRNFFVVLVL	180
QY	181	DYFSDTVYADLIIRLTGTGLEQLLVKOPKRLRDNYIHTQPKLDVASIIPDLYFAV	240
DB	181	DYFSDTVYADLIIRLTGTGLEQLLVKOPKRLRDNYIHTQPKLDVASIIPDLYFAV	240
QY	241	GIHSPVRFNRLHFARMPEFFDRTETRTSYNPIFFISNLVLVILVIHWNACIYYVISK	300
DB	241	GIHSPVRFNRLHFARMPEFFDRTETRTSYNPIFFISNLVLVILVIHWNACIYYVISK	300
QY	301	SIGFGVDTWYPIITDPEGYLAREYIYCLYNSTLTITIGETPPPVKDEEYLVFDFEL	360
DB	301	SIGFGVDTWYPIITDPEGYLAREYIYCLYNSTLTITIGETPPPVKDEEYLVFDFEL	360
QY	361	IGVLIIFATIVGVNISMNNATRAEFOAKIDAVKYMOPRKVSKDWEAKVVKFDFLWT	420
DB	361	IGVLIIFATIVGVNISMNNATRAEFOAKIDAVKYMOPRKVSKDWEAKVVKFDFLWT	420
QY	421	NKKTVDEREVLKMLPAKLRAEIAINVHLSTIKKVRIFQDWEAGLVVLKLRPQVSPG	480
DB	421	NKKTVDEREVLKMLPAKLRAEIAINVHLSTIKKVRIFQDWEAGLVVLKLRPQVSPG	480

Db 421 NKKTVDEREVLKLPKLAERAEIAINVHLSLTKKVRIFQDCEAGLLVELVLKLRPQVSPG 480
 QY 481 DYICRGDICKEMYIIKEGKLAIVADGVTOYALLSAGSCFGEISILINIKSGKMGNRRTAN 540
 Db 481 DYICRGDICKEMYIIKEGKLAIVADGVTOYALLSAGSCFGEISILINIKSGKMGNRRTAN 540
 QY 541 NIRSGLYSDFCLSKDDLMBAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQ 600
 Db 541 NIRSGLYSDFCLSKDDLMBAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQ 600
 QY 601 EKLEQLETNMDTLYTRFARLLAAYTGAQOKLKORIIVLETKMKQNHEDDYLSDGINTPEP 660
 Db 601 EKLEQLETNMDTLYTRFARLLAAYTGAQOKLKORIIVLETKMKQNHEDDYLSDGINTPEP 660
 QY 661 TAAE 664
 Db 661 TAAE 664

RESULT 2
 S35691
 Cyclic nucleotide-gated channel protein - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
 C:Accession: S35691
 R:Biel, M.; Altenhofen, W.; Hullin, R.; Ludwig, J.; Freichel, M.; Flockerzi, V.; Dascal, F.EBS Lett. 329, 134-138, 1993
 A:Title: Primary structure and functional expression of a cyclic nucleotide-gated channel
 A:Reference number: S35691; MUID:93359035; PMID:7689061
 A:Accession: S35691
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-732 <BI>
 A:Cross-references: EMBL:X59668; NID:q433959; PIDN:CAA42201.1; PID:q433960
 C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
 F:522-646/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 93.0%; Score 3231.5; DB 2; Length 732;
 Best Local Similarity 93.8%; Pred. No. 1.7e-219;
 Matches 622; Conservative 16; Mismatches 24; Indels 1; Gaps 1;

QY 2 MTEKNGVKSSPANNHHPPPSIKANGKDDHRRAGSRPOSVAADDTSELOQLAEMDTP 61
 Db 69 MTEKNGVKSSPANNHHVPAIKANGKDESRTSRPOS-AADDTSELOQLAEMDAP 127
 QY 62 RRGRGGFORIVRLGVIRDWANKNFRPEPRPDSFLERFRGPELQTVTTTHQDGGKDG 121
 Db 128 QQRGGFRIVRLGVIRDWANKNFRPEPRPDSFLERFRGPELQTVTTTHQDGGKDG 187
 QY 122 EKGTKKKFELFVLDPAQDWYRWLFVIAAMPVLYNWCLLVARACFSDLQRYFVWLVLD 181
 Db 188 DKGTKKKFELFVLDPAQDWYRWLFVIAAMPVLYNWCLLVARACFSDLQRYFVWLVLD 247
 QY 182 YFSDTVYIADLIIRLTGTGLEQGLAVKDPKLRDNYIHTLOPKLDVASIIPDLYFVAG 241
 Db 248 YFSDVYIADLIIRLTGTGLEQGLAVKDPKLRDNYIHTLOPKLDVASIIPDLYFVAG 307
 QY 242 IHSPEVRFNRLHFAFMFEFFDTRTSYPNIFRISNLVLYLVIHWNACIYVVISKS 301
 Db 308 IHNPEVRFNRLHFAFMFEFFDTRTSYPNIFRISNLVLYLVIHWNACIYVVISKS 367
 QY 302 IGFGVDTWYVNIPTDEYGLAREYIYCLYWSLTLLTTIGETPPPVKDEYLFVIFDFLI 361
 Db 368 IGFGVDTWYVNIPTDEYGLAREYIYCLYWSLTLLTTIGETPPPVKDEYLFVIFDFLI 427
 QY 362 GVLIIFATIVGNVSMISNNMNAEFAQAKIDAVKHYMQFRKVKSKMEAKVWKDFYLTWN 421
 Db 428 GVLIIFATIVGNVSMISNNMNAEFAQAKIDAVKHYMQFRKVKSKMEAKVWKDFYLTWN 487
 QY 422 KKTVDREVLKLPKLAERAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKLRPQVSPG 481
 Db 488 KKTVDREVLKLPKLAERAEIAINVHLSLTKKVRIFQDCEAGLLVELVLKLRPQVSPG 547

QY 482 YICRKDICKEMYIIKEGKLAIVADGVTOYALLSAGSCFGEISILINIKSGKMGNRRTAN 541
 Db 548 YICRKDICKEMYIIKEGKLAIVADGVTOYALLSAGSCFGEISILINIKSGKMGNRRTAN 607
 QY 542 IIRSLGYSDFCLSKDDLMBAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQ 601
 Db 608 IIRSLGYSDFCLSKDDLMBAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQ 667
 QY 602 KLEQLETNMDTLYTRFARLLAAYTGAQOKLKORIIVLETKMKQNHEDDYLSDGINTPEP 661
 Db 668 KLEQLETNMDTLYTRFARLLAAYTGAQOKLKORIIVLETKMKQNHEDDYLSDGINTPEP 727
 QY 662 AAE 664
 Db 728 AAE 730

RESULT 3
 S11521
 CAMP-gated channel protein - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
 C:Accession: S11521
 R:Ludwig, J.; Margalit, T.; Bismann, E.; Lancet, D.; Kaupp, U.B. F.EBS Lett. 270, 24-29, 1990
 A:Title: Primary structure of CAMP-gated channel from bovine olfactory epithelium.
 A:Reference number: S11521; MUID:91032022; PMID:1699793
 A:Accession: S11521
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-663 <LU>
 A:Cross-references: GB:X55010; NID:q287743; PIDN:CAA38754.1; PID:q287744
 C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
 F:454-578/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 92.2%; Score 3204.5; DB 2; Length 663;
 Best Local Similarity 92.3%; Pred. No. 1.2e-217;
 Matches 610; Conservative 27; Mismatches 23; Indels 1; Gaps 1;

QY 2 MTEKNGVKSSPANNHHPPPSIKANGKDDHRRAGSRPOSVAADDTSELOQLAEMDTP 61
 Db 1 MTEKANGVKSSPANNHHHAPPAIKASGKDDHRRASRPQSAIAA-DTTSSELQLAEMDAP 59
 QY 62 RRGRGGFORIVRLGVIRDWANKNFRPEPRPDSFLERFRGPELQTVTTTHQDGGKDG 121
 Db 60 QQRGGFRIVRLGVIRDWANKNFRPEPRPDSFLERFRGPELQTVTTTHQDGGKDG 119
 QY 122 EKGTKKKFELFVLDPAQDWYRWLFVIAAMPVLYNWCLLVARACFSDLQRYFVWLVLD 181
 Db 120 EKGTKKKFELFVLDPAQDWYRWLFVIAAMPVLYNWCLLVARACFSDLQRYFVWLVLD 179
 QY 182 YFSDTVYIADLIIRLTGTGLEQGLAVKDPKLRDNYIHTLOPKLDVASIIPDLYFVAG 241
 Db 180 YFSDVYIADLIIRLTGTGLEQGLAVKDPKLRDNYIHTLOPKLDVASIIPDLYFVAG 239
 QY 242 IHSPEVRFNRLHFAFMFEFFDTRTSYPNIFRISNLVLYLVIHWNACIYVVISKS 301
 Db 240 IHNPEVRFNRLHFAFMFEFFDTRTSYPNIFRISNLVLYLVIHWNACIYVVISKS 299
 QY 302 IGFGVDTWYVNIPTDEYGLAREYIYCLYWSLTLLTTIGETPPPVKDEYLFVIFDFLI 361
 Db 300 IGFGVDTWYVNIPTDEYGLAREYIYCLYWSLTLLTTIGETPPPVKDEYLFVIFDFLI 359
 QY 362 GVLIIFATIVGNVSMISNNMNAEFAQAKIDAVKHYMQFRKVKSKMEAKVWKDFYLTWN 421
 Db 360 GVLIIFATIVGNVSMISNNMNAEFAQAKIDAVKHYMQFRKVKSKMEAKVWKDFYLTWN 419
 QY 422 KKTVDREVLKLPKLAERAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKLRPQVSPG 481
 Db 420 KKSVDREVLKLPKLAERAEIAINVHLSLTKKVRIFQDCEAGLLVELVLKLRPQVSPG 479
 QY 482 YICRKDICKEMYIIKEGKLAIVADGVTOYALLSAGSCFGEISILINIKSGKMGNRRTAN 541

Db 480 YTCRKGDIKEMYYIIKEGKLVAVDDGVTVQYALLSAGSCFGEISILNIKSGMNRRTAN 539

QY 542 IRSLGYSDFCLSKODLMEAVTEAPDAKVKLEERGREILMKGLDENVAASMEVDVDE 601

Db 540 IRSLGYSDFCLSKODLMEAVTEAPDAKVKLEERGREILMKGLDENVAASMEVDVDE 599

QY 602 KLEQLETNMDTLTYTRFARLLAAYTGAAQKLKORITVLETKMKQNHDDYLSGINTPEPT 661

Db 600 KLEQLETNMDTLTYTRFARLLAAYTGAAQKLKORITVLETKMKQNHDDYLSGINTPEPT 659

QY 662 A 662

Db 660 A 660

RESULT 4

I50630

alpha subunit of cone photoreceptor CNG-channel - chicken

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999

C:Accession: I50630

R:Bonigk, W.; Altenhofen, W.; Muller, F.; Dose, A.; Illing, M.; Molday, R.S.; Kaupp, U.B. Neuron 10, 865-877, 1993

A:Title: Rod and cone photoreceptor cells express distinct genes for cGMP-gated channels

A:Reference number: I50630; MUID:93264082; PMID:7684234

A:Accession: I50630

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-735 <BON>

A:Cross-references: EMBL:X89598; NID:9908850; PIDN:CAA61757.1; PID:9908851

C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-F:524-648/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 63.9%; Score 2219.5; DB 2; Length 735;

Best Local Similarity 59.4%; Pred. No. 3e-148;

Matches 42; Conservative 93; Mismatches 113; Indels 89; Gaps 7;

QY 16 NNNHHPPP---SIKANGKDDHFRAGS---RPQSVAAADDDTSPELQRLAEMD----- 59

Db 5 NTOHSYFGMHGLSVRTTDEIERENGFIKTHSLC--EDTSSELQVISMEGRHLSGSQT 62

QY 60 TPRRGHGQFQIVRLMGVIRDWANKNFRPEPRPDSFLERFRGPELQTVTHQG----- 113

Db 63 SPFTGRGAMARLSRFVVSLSRWATRLHHDDQRPDSFLERIRGPELVEVSSRQSNIRSF 122

QY 114 -----D 114

Db 123 GIREQGVNWPFLARFVNFSNNTNEDKKEKKEKKEKKEKKEKKEKKEKDDKDDK 182

QY 115 DKGGKDGEGKTKKKKPELVDPAGDWYRWLFVIAFPVLYNWLIVARACFSDLQRYN 174

Db 183 KKDDKKDDKKKEQKEVEFVDPSSNMVYNNWLTIAAPVFNWMLICRACFDELQIDHI 242

QY 175 VVWLVLVDFSDTVYIADLIIRLTGLEQGLVADPKKLDNDYIHTLOKLDVASIIP 234

Db 243 KWLFDYICSDIIVDFMFRFTGLEQGLLVKDEKLDHDTYQTVQFKLDVLSLPTD 302

QY 235 LIYFAVGIIHSPVFRNRLHLPARMFFORTERTSYNIFRISNLVILVLIHWNACI 294

Db 303 LAYKLGLNYPFLRNRLHLPARMFFORTERTSYNIFRISNLVILVLIHWNACI 362

QY 295 YVWISKISGVDTWYVYNTIDPEYGLAREYIYCYLWSTLTITIGETPPPVKDEYLF 354

Db 363 YFAISKVIGFSDWVYVNVISPEYGRLSKYIYSLWSTLTITIGETPPPVKDEYLF 422

QY 355 VIEDELIGLIVATIVGNVSMISNNNATPAEQAKIDAVKHYQFRKYSKDEAKVIKW 414

Db 423 VVDFLVGLVLIIVATIVGNVSMISNNNATPAEQAKIDAVKHYQFRKYSKDEAKVIKW 482

QY 415 FDLWLNKTKVDERVLKDLPAKRAEIALNVHLSLTKKVRIFQDWEAGLLVVLKLRP 474

Db 483 FDLWLNKTKVDEKVLKDLPAKRAEIALNVHLSLTKKVRIFQDWEAGLLVVLKLRP 542

QY 475 QVFSFGDYTCRKGDIKEMYYIIKEGKLVAVDDGVTVQYALLSAGSCFGEISILNIKSGM 534

Db 543 TVFSFGDYTCRKGDIKEMYYIIKEGKLVAVDDGVTVQYALLSAGSCFGEISILNIKSGS 602

QY 535 GNRRTANIRSLGYSDFCLSKODLMEAVTEAPDAKVKLEERGREILMKGLDENVAAS 594

Db 603 GNRRTANIRSLGYSDFCLSKODLMEAVTEAPDAKVKLEERGREILMKGLDENVAAS 662

QY 595 ME-VDVQEKLEOLEFNMDTLTYTRFARLLAAYTGAAQKLKORITVLETKMKQNHDDYLS 653

Db 663 ADPKOLEEKIDRLTDLTQTRFARLLAAYSSSQKVKQRLARVETRVKK-----YGS 717

QY 654 GINTPEP 660

Db 718 SLSVGE 724

RESULT 5

A55251

cyclic nucleotide-gated Ca++ channel protein CNM-3 - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 13-Aug-1999

C:Accession: A55251; S43976

R:Biel, M.; Zong, X.; Distler, M.; Bosse, E.; Klugbauer, N.; Murakami, M.; Flockerzi, V. Proc. Natl. Acad. Sci. U.S.A. 91, 3505-3509, 1994

A:Title: Another member of the cyclic nucleotide-gated channel family, expressed in tes

A:Reference number: A55251; MUID:94224768; PMID:8170936

A:Accession: A55251

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-706 <BIE>

A:Cross-references: GB:X76485; NID:9488728; PIDN:CAA54023.1; PID:9488729

A:Experimental source: kidney

R:Weyand, I.; Godde, M.; Frings, S.; Weiner, J.; Mueller, F.; Altenhofen, W.; Hatt, H.; Nature 368, 859-863, 1994

A:Title: Cloning and functional expression of a cyclic nucleotide-gated channel from me

A:Reference number: S43976; MUID:94211295; PMID:7512693

A:Accession: S43976

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-706 <WEY>

A:Cross-references: GB:X89600; NID:9908823; PIDN:CAA61759.1; PID:9908824

A:Experimental source: testis

C:Genetics:

A:Gene: CNM3

C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide

C:Keywords: cGMP binding; ion channel; ion transport; membrane protein

F:501-625/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 61.6%; Score 2140; DB 2; Length 706;

Best Local Similarity 60.4%; Pred. No. 1.1e-142;

Matches 419; Conservative 94; Mismatches 119; Indels 62; Gaps 7;

QY 11 SSPANNHNNHPPSPISKANGKD--DHAGSRPQSVQVADDDTSPELQRLAEMDTPRGSG--- 66

Db 9 SHPTRETH-----PSVRTMDRLDCIENGSLRTHLPEETSSSELQEGIAMET--RGLAESR 61

QY 67 -----GFQIVRLVGVIRDWANKNFRPEPRPDSFLERFRGPELQTVTHQG----- 113

Db 62 QSSFTSQGTSLRSLRLIISLRASARHLHDDQRPDSFLERFRGPELQTVTHQG----- 121

QY 114 -----DDKGGKDG-----GKTKKKKPELVLD 136

Db 122 GSQEPDPRGRSAWPLARNNTNTCNNSEKDDKAKKEKKEKKEKKEKKEKKEKSDVMD 181

QY 137 PAGDWYRWLFVIAFPVLYNWLIVARACFSDLQRYNFWVWLVDYFSDTVIADLIIRL 196

Db 182 PPSNMYIHWLTIVIAFVFNWCLVCRACFDELQSEHLMLWLVDYSDILYGMMLVRA 241

QY 197 RTGLEQGLVADPKKLDNDYIHTLOKLDVASIIP 256

Db 242 RTGLEQGLVADPKKLDNDYIHTLOKLDVASIIP 301

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QY 257 RMFEFDRTRTSTSYNIFRIENLVLIIVIIHWNACIYVVISKSGFVGDTWVYPTND 316
DB 302 RLEFEFDRTRTSTSYNIFRIENLVLIIVIIHWNACIYVVISKSGFVGDTWVYPTNS 361
QY 317 PSYGLARYIYCLVWSTLTTLTIGTPTPPVDEEYLVFVIFDLGLVLFATVGNVGM 376
DB 362 PSYGLRSRYIYSLVWSTLTTLTIGTPTPPVDEEYLVFVIFDLGLVLFATVGNVGM 421
QY 377 ISNMNATREFOAKIDAVKHVMQFRVSKDMKAKVTKWFDYLTWNTKKTVDREVKNLPA 436
DB 422 ISNMNATREFOAKIDSIYQYQWFRVTKDLETRVIRWFDYLVWANKKTVDREVKLSLPD 481
QY 437 KLRAEAIINVHSLTKKVRIFQDWEAGLLVELVLKLPQVFPSPGDYICRKGDIKEMYYII 496
DB 482 KLKAEAIINVHSLTKKVRIFQDCEAGLLVELVLKLPVAFSPGDYICKKGDIKEMYYII 541
QY 497 KEGKLAIVADDGVTQVALLSAGSCFGEISILNIKSGKMGNNRRTANIRSIYSDLPCLSKD 556
DB 542 KEGKLAIVADDGVTQVALLSAGSCFGEISILNIKSGKMGNNRRTANIRSIYSDLPCLSKD 601
QY 557 DLMEAVTEAPDAKVLLEERGREILMKWGLLDENEVAASME-VDVQEKLEQLETNMDTLTYT 615
DB 602 DLMEAVTEAPDAKVLLEERGREILMKWGLLDENEVAASME-VDVQEKLEQLETNMDTLTYT 661
QY 616 RFARLLAEXTGAQOKLKQRTVLETKVQKQNHDD 649
DB 662 RFARLLAEXTGAQOKLKQRTVLETKVQKQNHDD 695

RESULT 6
JH0560
cyclic nucleotide-gated channel - channel catfish
C:Species: Ictalurus punctatus (channel catfish)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0560
A:Title: Molecular cloning and single-channel properties of the cyclic nucleotide-gated
A:Reference number: JH0560; MUID:92110008; PMID:1370374
A:Accession: JH0560
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-682 <GOU>
A:Cross-references: GB:M83111
A:Experimental source: olfactory epithelium
A:Comment: This cyclic nucleotide-gated channel is activated equally well by both cAMP and
A:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
C:Keywords: cAMP binding; cGMP binding; ion channel; ion transport; olfaction; transmembr
F:137-157/Domain: transmembrane #status predicted <TS1>
F:173-193/Domain: transmembrane #status predicted <TS2>
F:217-236/Domain: transmembrane #status predicted <TS3>
F:241-261/Domain: transmembrane #status predicted <TS4>
F:277-297/Domain: transmembrane #status predicted <TS5>
F:319-337/Domain: transmembrane #status predicted <TS6>
F:350-370/Domain: transmembrane #status predicted <TS6>
F:447-571/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 61.3%; Score 2131; DB 1; Length 682;
Best Local Similarity 67.7%; Pred. No. 4.6e-142;
Matches 419; Conservative 68; Mismatches 110; Indels 22; Gaps 6;

QY 34 RAGRFQSVAAADDTSPQLAEMDTPR-----RGRGGFORIVRLVGVIRDWANKNF 86
DB 28 RAESAISRTDGGDDTSCSQRLVTALELPSAEMLEAFQRRPLARLVNLVLSREWAKSL 87
QY 87 REEPSPDSFLERFRGPELQTVTHQDDKGG--KDEGKGTKKKPELVFLDPAGDWYR 144
DB 88 VETEQRPSFLERFRGQ-----AANDQSAAPADAPKTKFERMEGFVVSQDIYY 140
QY 145 WLFVIRAMPVLYNCLLVARACFSDLRQRYFVWVLVDYFSDTVVIADLIIRLTGFLQEG 204
DB 141 WLFVIRAMPVLYNCLLVARACFSDLRQRYFVWVLVDYFSDTVVIADLIIRLTGFLQEG 200

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QY 205 LLVKDPKKLRDNYIHTLOFKLDVASIIPTDLIYFAVGIHSPVRENRLLHPRMFEFFDR 264
DB 201 LLVKDLAKLRDNYIHTLOFKLDVASIIPTDLIYFAVGIHSPVRENRLLHPRMFEFFDR 259
QY 265 TETRTSYNIFRIENLVLIIVIIHWNACIYVVISKSGFVGDTWVYPTNDTPEYGYLAR 324
DB 260 TETRTSYNIFRIENLVLIIVIIHWNACIYVVISKSGFVGDTWVYPTNDTPEYGYLAR 315
QY 325 EYIYCLVWSTLTTLTIGTPTPPVDEEYLVFVIFDLGLVLFATVGNVGMISNNMTR 384
DB 326 EYIYCLVWSTLTTLTIGTPTPPVDEEYLVFVIFDLGLVLFATVGNVGMISNNMTR 375
QY 385 AEFQAKIDAVKHVMQFRVSKDMKAKVTKWFDYLTWNTKKTVDREVKNLPAKRAEAI 444
DB 376 AEFQAKIDAVKHVMQFRVSKDMKAKVTKWFDYLTWNTKKTVDREVKNLPAKRAEAI 435
QY 445 NVHLSTLKKVRIFQDWEAGLLVELVLKLPQVFPSPGDYICRKGDIKEMYYIIKEQGLAVV 504
DB 436 NVHLSTLKKVRIFQDCEAGLLVELVLKLPQVFPSPGDYICRKGDIKEMYYIIKEQGLAVV 495
QY 505 ADDGVTQVALLSAGSCFGEISILNIKSGKMGNNRRTANIRSIYSDLPCLSKDLMVAE 564
DB 496 ADDGVTQVALLSAGSCFGEISILNIKSGKMGNNRRTANIRSIYSDLPCLSKDLMVAE 555
QY 565 APDAKVLLEERGREILMKWGLLDENEVAASMEV-DVQEKLEQLETNMDTLTYTRFARLLAE 623
DB 556 YPDAKVLLEERGREILMKWGLLDENEVAASMEV-DVQEKLEQLETNMDTLTYTRFARLLAE 615
QY 624 YTGAKOKLKQRTVLETKM 642
DB 616 FTSTQRLKQRTALERQL 634

RESULT 7
S74179
cyclic nucleotide-gated channel protein - human
C:Species: Homo sapiens (man)
C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 16-Jul-1999
C:Accession: S74179
A:Title: Molecular cloning, functional expression and chromosomal localization of a hum
A:Reference number: S74179; MUID:96409310; PMID:8814292
A:Accession: S74179
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-695 <YUW>
A:Experimental source: retina
C:Genetics:
A:Map position: 2
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide
C:Keywords: ion channel; ion transport; membrane protein
F:482-607/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 61.2%; Score 2126.5; DB 2; Length 695;
Best Local Similarity 61.5%; Pred. No. 9.9e-142;
Matches 429; Conservative 92; Mismatches 130; Indels 47; Gaps 11;

QY 5 KNGVKSPANNHHPPSIKANGKDDHRAG---SRQSVAAADDTSPQLAEMDTP- 60
DB 3 KINTQVSHPSRTH-----LEVKTSDRLNRAENGJSRAHS---SSSETSVLPQGTAMEYR 55
QY 61 --PRGRG-----GFORIVRLVGVIRDWANKNFREPRPDSFLERFRGPELQTVTHQG 113
DB 56 GLADSGQSFTQGIARLSRLIFLLRWAARVHHQDQGPSFDPFRFGAELKEVSSQES 115
QY 114 D-----DKG-----GKDGKGTKKKPELVFLDPAGDWYRFLV 148
DB 116 NQAQNVGSOEADRGSAWPLAKCNTNTSNTEEEKTKKK-DAIVDPSSNLYRRLTA 174
QY 149 IAMPVLYNCLLVARACFSDLRQRYFVWVLVDYFSDTVVIADLIIRLTGFLQGLVAK 208
DB 175 IALPFYNNYLLICRACFDELOSEYIMLMVLVDYFSDTVVIADLIIRLTGFLQGLVAK 234

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QY 209 DPKLRDNYIHTLOKLDVASIIPDLYIFAVGIHSPEVRENFLLHFAFMFEFFDRTETR 268
Db 235 DYNRLMCHYKTTQFKLDVLSLPTDLAYLKVGNTYPEVRENFLLKFSRLFFEDRTETR 294
QY 269 TSPYNI FRISNLVLYLIIHWNACIYVVISKSGFVDTWYYPNITDPEYGYLAREYIY 328
Db 295 TYPNMFRI GNLVLYLIIHWNACIYFALSKEFGTDSWYYPNISIPHGRLSRKIY 354
QY 329 CLYWSLTITTTGETPPPKVDEYLFIYDFDLGLVLI FATIYGVGSMISNNMATAEFQ 388
Db 355 SLYWSLTITTTGETPPPKVDEYLFVVDVFLVGLVLI FATIYGVGSMISNNMATAEFQ 414
QY 389 AKIDAVKHYMQPKVSKVMEAKVIKFDYLTWTKTVDRREVILKNIPLAKIRABIAINVLH 448
Db 415 AKIDSIKQYMQPKVTKDLETRVIRFVDFYLVANKTVDEKEVLSKLPDKLKAELAINVLH 474
QY 449 STLKVRIFQDWEAGLLVELVLKLRQVPFSPGYDI CRKGDIGKEMVIIKEGKLAVVADGG 508
Db 475 DTLKVRIFQDCEAGLLVELVLKLRPTVFPSPGYDI CKGDI GEMVIIKEGKLAVVADGG 534
QY 509 VTQYALLSAGSCFGEISILNIKSGKMGNTANIRSIGYSDLFCLSKDLMLEAVTEAP-D 567
Db 535 VTQFVLSGSGYFGEISILNIKSGKMGNTANIRSIGYSDLFCLSKDLMLEALTYPGQ 594
QY 568 AKKVLREGR EILMKMGLLDENEVAASME--VDVQEKLEQLETNMDTLITRFARLLAAYTG 626
Db 595 AKKALEKGRQILMKDNLIDELARAGADPKDLEEKVQGLSGSLDTLQTFARLLAAYNA 654
QY 627 AQOKLKQRTVLTETKMKQNHEDDYLSGINTPEPTAAE 664
Db 655 TOMMKQRLSQLESQVK--GGGDPLADGEVPGDATKTE 691

RESULT 8
150680
alpha subunit of rod photoreceptor CNM-channel - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C:Accession: I50680
R;Bonigk, W.; Alenchofen, W.; Muller, F.; Dose, A.; Illing, M.; Molday, R.S.; Kaupp, U.H.
Neuron 10, 865-877, 1993
A;Title: Rod and cone photoreceptor cells express distinct genes for cGMP-gated channels
A;Reference number: I50630; MUID:93264082; PMID:7694234
A;Accession: I50680
A;Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A;Residues: 1-645 <EON>
A;Cross-references: EMBL:X89599; NID:9908852; PIDN:CAA61758.1; PID:9908853
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
F;431-555/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 59.5%; Score 2067; DB 2; Length 645;
Best Local Similarity 62.9%; Pred. No. 1.4e-137;
Matches 406; Conservative 78; Mismatches 123; Indels 38; Gaps 6;

QY 19 HPPPPSIKANGKODHRAGSRPQSVAAADDDTSPELQRLAEMDTPRGRGGFQIRVLVGV 78
Db 9 HHSHPII-----PSVVVQTSDDPGL-----IEKGNRRFARQWYLPGAF 47

QY 79 -----RDWANKNFRBEEPPDPSFLERFRGPPELQTVTTHQGDGKGKGKGTKK 128
Db 48 AQYNINNNNSKKDEKKKKKSKSENKKDGERQKNEKKHKKDK-----KKGKEEK 103

QY 129 KFELVLDPADGWYRMLFVIAMPVLYNWCLLVARACFSDLORNYFVWLVLDYFSDTVY 188
Db 104 KQIFIIDPAGMYNNWLFCTLPMYNNWNTMIARACFDELQNDYLAWFWFVYVSVITY 163

QY 189 IADLIIRLTGFLRQGLLVKDPKKLRDNYIHTLOKLDVASIIPDLYIFAVGIHSPEVR 248
Db 164 IADMVTRTGLYRQGLLVKEEQKLKEKYSLSLQKLDLFLSIITDLYLFGKGLNYFELR 223

QY 249 FNLHLHFAFMFEFFDRTETRTPSYNIFRISNLVLYLIIHWNACIYVVISKSGFVDT 308

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Db 224 INRLLEVAEMFEFFDRTETRTPSYNIFRISNLVLYLIIHWNACIYVVISKSGAGDT 283
QY 309 WYYPNITDPEYGYLAREYIYCYWSTLTITTTGETPPPKVDEYLFIYDFDLGLVLI F 368
Db 284 WYYPNTSHPEFFARLTRKYVYSLYWSTLTITTTGETPPPVDRDSEYFFVVDVFLVGLI F 343
QY 369 IVGNVGSMSNNMATAEFQAKIDAVKHYMQPKVSKVMEAKVIKFDYLTWTKTVDR 428
Db 344 IVGNVGSMSNNMATAEFQAKIDAIKQYHFNVSQKMEKVIKFDYLTWTKTVDR 403
QY 429 EYLNKLPKAKIRAEIAINVLHSTLTKVRIFQDWEAGLLVELVLKLRQVPFSPGYDI CRKGD 488
Db 404 EYLVKLPDKLRAEIAINVLHSTLTKVRIFADCEAGLLVELVLKLRQVPFSPGYDI CRKGD 463
QY 489 IGKEMVIIKEGKLAVVADGGVTQYALLSAGSCFGEISILNIKSGKMGNTANIRSIGYS 548
Db 464 IGKEMVIIKEGKLAVVADGGVTQFVLSGSGYFGEISILNIKSGKMGNTANIRSIGYS 523
QY 549 DLFCLSKDLMLEAVTEAPDAKKVLEERGREILMKMGLLDENEVA--ASMEVDVQEKLEQ 606
Db 524 DLFCLSKDLMLEALTEYPPAKAMLEKKGKQLMKDGLLD-IEVANLGSPPKOLEEKVAYM 582
QY 607 ETNMDTLITRFARLLAAYTGAQOKLKQRTVLTETKMKQNHEDDYL 651
Db 583 EGSMDRLQTKFARLLAAYDAAQOKLKRLTQIEKILKPVMEQDFL 627

RESULT 9
S07103
cGMP-gated ion channel protein - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S07103
R;Kaupp, U.B.; Miodome, T.; Tanabe, T.; Terada, S.; Boenigk, W.; Stuehmer, W.; Cook, N.
Nature 342, 762-766, 1989
A;Title: Primary structure and functional expression from complementary DNA of the rod
A;Reference number: S07103; MUID:90098076; PMID:2481236
A;Accession: S07103
A;Status: not compared with conceptual translation
A:Molecule type: mRNA
A;Residues: 1-690 <NAU>
A;Cross-references: GB:X51604; NID:9203; PIDN:CAA35947.1; PID:9204
C;Note: part of this sequence was confirmed by protein sequencing
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
C;Keywords: cGMP binding; eye; ion channel; ion transport; retina; transmembrane protei
F;477-601/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 58.8%; Score 2044; DB 1; Length 690;
Best Local Similarity 63.5%; Pred. No. 6.3e-136;
Matches 401; Conservative 82; Mismatches 118; Indels 30; Gaps 7;

QY 41 SVAADDDTSPELQRLAEMDTPRGRGGF-----QIRVLVGVIR--DWANKNER 87
Db 37 SFGSDDDDSGASMPFESEETNP-HARDSFRSNTHGSGSQSQREQLPGAIALFNWNSSNK 95
QY 88 EEEPP-----RPSDFLERFRGPPELQTVTTHQGDGKGKGKGTGK--KKFELF 133
Db 96 EQEPKPKKKKKKKKKKSKPKDKNKKDPE-KKKKKKKKKKKKKKKKKKKKKKKKKKKKK 154
QY 134 VLDPADGWYRMLFVIAMPVLYNWCLLVARACFSDLORNYFVWLVLDYFSDTVIADLI 193
Db 155 VIDPSGNTYNNWLFCTLPMYNNWNTMIARACFDELQSDYLEYWLAFDYLSDVYLLDMF 214
QY 194 IRLRTGFLRQGLLVKDPKKLRDNYIHTLOKLDVASIIPDLYIFAVGIHSPEVRNRL 253
Db 215 VRTRTGFLRQGLLVKDEKRLDKYKSTTFQKLDVLSVIPDLYIIFKGMNPIRLNRL 274
QY 254 HFARMEFFDRTETRTPSYNIFRISNLVLYLIIHWNACIYVVISKSGFVDTWYYPN 313
Db 275 RISRMFEFFDRTETRTPSYNIFRISNLVLYLIIHWNACIYVVISKSGFVDTWYYPD 334
QY 314 ITDPEYGYLAREYIYCYWSTLTITTTGETPPPKVDEYLFIYDFDLGLVLI F 373

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354 FVIFDFLIGVLIFATIVGNVSMISNMNATRAEFOAKIDAVKHYMQFRKYSKMEAKVIK 413
377 FVVVDLIGVLIFATIVGNVSMISNMNATRAEFOAKIDAVKHYMQFRKYSKMEAKVIK 436
414 WFDYLTWNTKKTVDREVLKNIIPAKLRAEIAINVHLDTLKKVRIPODWEAGLLVBLVKLR 473
437 WFDYLTWNTKKTVDREVLKNIIPAKLRAEIAINVHLDTLKKVRIPODWEAGLLVBLVKLR 496
474 PQVSPGDYICRKGDIKEMYYIKKEGLAVVADGGVTCYALLSAGSCFGEISILNIKSGK 533
497 PQVSPGDYICRKGDIKEMYYIKKEGLAVVADGGVTCYALLSAGSCFGEISILNIKSGK 556
534 MGNRRRTANIRSLGYSDFCLSKDDLMBAVTEAPDAKVKLEERGREGREILMKMGLLDENEV-A 592
557 AGNRRRTANIRSLGYSDFCLSKDDLMBAVTEAPDAKVKLEERGREGREILMKMGLLDENEV-A 616
593 ASNEVDVQEKLEQLENTMDLYTRFARLLAETGAQOKLKQRIITVLETKMKQNHEDDYL 652
617 GSDPKDLEEKVTRMEGSDVLLQTRFARILAEYESMOOKLKQRLTKVERFLKPLIDTFSS 676

RESULT 12
JC6509
rod cyclic nucleotide-gated cation channel protein alpha-chain - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
A;Accession: JC6509
R;Veske, A.; Nilsson, S.E.G.; Gal, A.
Gene 202, 115-119, 1997
A;Title: Characterization of canine rod photoreceptor cGMP-gated cation channel alpha-subunit
A;Reference number: JC6509; MUID:98087425; PMID:9427553
A;Accession: JC6509
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-691 <VES>
A;Cross-references: EMBL:X99914; NID:g1488571; PIDN:CAA68186.1; PID:g1488572
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-binding domain
F;478-602/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 58.18; Score 2017.5; DB 2; Length 691;
Best Local Similarity 61.38; Pred. No. 4.6e-134;
Matches 398; Conservative 94; Mismatches 126; Indels 31; Gaps 7;

QY 23 PSITKANGKODHRAGSRPQSVAAAD---DTSPELQRLAEMDTPR-----RGGGFQR 70
DB 21 PDIE---KEIRRMENGARSFSDDDGDDGDSASMESENETPHARDSCRNNSQRDPDSQR 77
QY 71 IVPLVGVR--DWANKNFRPEPDPDSFLERFRGPELQTVTTHQGD-----DKG 117
DB 78 EQYLPGAIALFNVNNSNKEQEPKKEKKKKKKSGDKNENKDKSEKKKKKEKKEKK 137
QY 118 GKDGEGKGTG--KKFELFVLDPADGWYRWLFVIAMPVLYNWCLLVARACFSDIQRNYFV 175
DB 138 NKEEGKDKKEEKKEVWVIDPAGNMYNWLFCITLFPVYNWNTMIARACFDELQSDYLE 197
QY 176 VMLVLDYFSTVYIADLIIRLTGFLGQLLVKDPKKLRNYIHTLQFKLDVASIIPDIL 235
DB 198 YWIIFDYLSDIVLLDMFVTRTGYLEQGLLVREAAKLEIKYKSNLQFKLDFLSVPTDL 257
QY 236 IYFAVGHSPEVRPNLLHFARMEFPDRTETSYNIFRISNLVLIIVIIHWNACIY 295
DB 258 LYFKLGWNYPEIRNLRLIRSRMEFPQRTETRTNYNIFRISNLVLIIVIIHWNACIY 317
QY 296 YVTSKSGFGVDTWVYENITDPEYGLAREYIYCLYVSTLTLTIGTPPPVKDEEYLFV 355
DB 318 FSISKALGFGNDTWVYEDVNDPEFGLARKYVLSYVSTLTLTIGTPPPVKDSYV 377
QY 356 IFDFLIGVLIFATIVGNVSMISNMNATRAEFOAKIDAVKHYMQFRKYSKMEAKVIK 415
DB 378 VDFLIGVLIFATIVGNVSMISNMNATRAEFOAKIDAVKHYMQFRKYSKMEAKVIK 437
QY 416 DYLTWNTKKTVDREVLKNIIPAKLRAEIAINVHLDTLKKVRIPODWEAGLLVBLVKLR 475

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438 DYLTWNTKKTVDREVLKNIIPAKLRAEIAINVHLDTLKKVRIPODWEAGLLVBLVKLR 497
476 VFPSPGDYICRKGDIKEMYYIKKEGLAVVADGGVTCYALLSAGSCFGEISILNIKSGK 535
498 VFPSPGDYICRKGDIKEMYYIKKEGLAVVADGGVTCYALLSAGSCFGEISILNIKSGK 557
536 NRRRTANIRSLGYSDFCLSKDDLMBAVTEAPDAKVKLEERGREGREILMKMGLLDENEV-AAS 594
558 NRRRTANIRSLGYSDFCLSKDDLMBAVTEAPDAKVKLEERGREGREILMKMGLLDENEV-AAS 617
595 MEYDVOEKLEQLENTMDLYTRFARLLAETGAQOKLKQRIITVLETKMK 643
618 DPDKLEEKVTRMEGSDVLLQTRFARILAEYESMOOKLKQRLTKVERFLK 666

RESULT 13
B42161
cGMP-gated cation channel, rod photoreceptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999
C;Accession: B42161
R;Pittler, S.J.; Lee, A.K.; Altherr, M.R.; Howard, T.A.; Seldin, M.P.; Hurwitz, R.L.; &
J. Biol. Chem. 267, 6257-6262, 1992
A;Title: Primary structure and chromosomal localization of human and mouse rod photoreceptor cGMP-gated cation channel; cAMP receptor protein cyclic nucleotide-binding domain
A;Reference number: A42161; MUID:92210603; PMID:1372902
A;Accession: B42161
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-688 <PIT>
A;Cross-references: GB:M84742
A;Note: authors translated the codon TAT for residue 544 as Thr
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-binding domain
C;Keywords: cGMP binding
F;475-599/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 57.48; Score 1995.5; DB 2; Length 688;
Best Local Similarity 61.04; Pred. No. 1.6e-132;
Matches 398; Conservative 88; Mismatches 143; Indels 23; Gaps 6;

QY 21 PPSITKANGKODHRAGSRPQSVAAADDTSPQLQRLAEMDTPRGG-----RGGGFQRI 75
DB 20 PNIVIPAIEKEIRRMENGARSFSDDDGDDGDSASMESENETPHARDSCRNNSQRDPDSQR 79
QY 76 GV-----IRDWANKN-----FREEPRPDSFLERFRGPELQTVTTHQGD--DKGGK 119
DB 80 GTWALFNVNNSNKEQEPKKEKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 139
QY 120 DGEKGTGKKEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKEK 179
DB 140 TKEKKEKK--EVVVIDPSGNTYNNWLFCTLFPVYNWNTMIARACFDELQSDYLEWLI 198
QY 180 LDYFSTVYIADLIIRLTGFLGQLLVKDPKKLRNYIHTLQFKLDVASIIPDILYFA 239
DB 199 FDYVSNVYIADLMFVTRTGYLEQGLLVKDKRMKLEIKYKSNLQFKLDSVPTDLYIK 258
QY 240 VGHSPSEVFRNLLHFARMEFPDRTETSYNIFRISNLVLIIVIIHWNACIYVVIS 299
DB 259 FGWNYPEIRNLRLIRSRMEFPQRTETRTNYNIFRISNLVLIIVIIHWNACIYVIS 318
QY 300 KSGFGVDTWVYENITDPEYGLAREYIYCLYVSTLTLTIGTPPPVKDEEYLFVIFDF 359
DB 319 KALGFGNDTWVYEDVNDPEFGLARKYVLSYVSTLTLTIGTPPPVLDSEYIFVVVDF 378
QY 360 LIQVLIFATIVGNVSMISNMNATRAEFOAKIDAVKHYMQFRKYSKMEAKVIKWFYLM 419
DB 379 LIQVLIFATIVGNVSMISNMNATRAEFOAKIDAVKHYMQFRKYSKMEAKVIKWFYLM 438
QY 420 TNKTKTVDREVLKNIIPAKLRAEIAINVHLDTLKKVRIPODWEAGLLVBLVKLRPOV 479
DB 439 TNKTKTVDREVLKNIIPAKLRAEIAINVHLDTLKKVRIPODWEAGLLVBLVKLRPOV 498
QY 480 GDYICRKGDIKEMYYIKKEGLAVVADGGVTCYALLSAGSCFGEISILNIKSGKMG 539

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Db 499 GYICKKGGIGREMYIIKEGLAVAVADDGDTQFWLSDGSYFGEISILNKGSKAGNRRT 558
QY 540 ANIRSGYSLFCLSKDDLEAVEAPDAKKVLEERGRILLMKWGLLDENEV-AASMEVD 598
Db 559 ANIKSGYSLFCLSKDDLEVEITPDATKMLEEGRQLMKDGLLDINIAMGSDPKD 618
QY 599 VQPKLEQLETMTLTFRFARLLAEYTGAAQKLKQRIITVLETKMKQNHEDDY 650
Db 619 LEEKVTRMEGSDVLLQTRFACILAEYESMQOKLKQRLTKVEKFLKPIETEF 670
RESULT 14
I59327
Olfactory cyclic nucleotide gated cation channel - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Mar-2000
C:Accession: I59327, I58165
R:Bradley, J.; Li, J.; Davidson, N.; Lester, H.A.; Zinn, K.
Proc. Natl. Acad. Sci. U.S.A. 91, 8890-8894, 1994
A:Title: Heteromeric olfactory cyclic nucleotide-gated channels: A new subunit that confers high
A:Reference number: I59327; MUID:94377458; PMID:7522325
A:Accession: I59327
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-575 <RES>
A:Cross-references: EMBL:U12623; NID:G538128; PIDN:AAA21464.1; PID:G538129
R:Limán, B.R.; Buck, L.B.
Neuron 13, 641-621, 1994
A:Title: A second subunit of the olfactory cyclic nucleotide-gated channel confers high
A:Reference number: I58165; MUID:95000663; PMID:7522482
A:Accession: I58165
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-575 <RE2>
A:Cross-references: EMBL:U12425; NID:G548083; PIDN:AAA64748.1; PID:G548084
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
F:348-472/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
Query Match 43.7%; Score 1518; DB 2; Length 575;
Best Local Similarity 53.8%; Pred. No. 5.3e-99;
Matches 290; Conservative 101; Mismatches 142; Indels 6; Gaps 2;
QY 126 TKKKFELVLDPAQDGYWYRWLFVAMPVLYNWCLLVARACFSDLQRYFVWLVLDYFSD 185
Db 18 TRARKLPVLDPSGDYIYWNLTWTFPIYMYNLIIYVCRACFPDLOHSLYVWAFVLDYTS 77
QY 186 TVYIADLIIRLGRFLEQGLLVKDPKKLRDNYHTLQKLDVASIIPDLYFAVGHS 245
Db 78 LLYLLDYGVRFHGTGLEQGLLVVDKGMASRYRTWSTFLLDLSLVPTDAAYVOLGPHIP 137
QY 246 EVFENRLLHFAEFDFDRTETSTYFNIRISNLVLYILVLIHWNACIYVVISKSGIFG 305
Db 138 TLRLNRFRLVRPFEAFDRTEATAYENAPRIAKMLIYFVVIHWNACIYVVISKSGIFG 197
QY 306 VDTWYVNTDPEYGLAREYIYCLWSTLTITIGETPPVKDEBYLFVIFDPLGLVLI 365
Db 198 RDWVTPDPAQFERLRQKLYSFFSTLITLTGDTPLPDEBYLFVWVGDFLLAVMG 257
QY 366 FATVGNVSGSMINMNATRAEFOAKIDAVKHVMQFRKVKSDMEAKVIKWFVLYLWTKTKV 425
Db 258 FATIMSGSMVINYMTADAAFPDHALVKYMKLQHVNKRLERRVIDWVQHLQINKKMT 317
QY 426 DERVLKNLPKARAEIAINVHLSLTKKVRIFODWBAGLLVEILKLRPQVFSFGYICR 485
Db 318 NEVAAILQHLPERLRAEVAVSVHLSLTSRVQFQCEASLLEELVLLKLPQTYSPGEYVCR 377
QY 486 KGDIGKEMYLIIKEGLAVAVDDGVTQYALLSAGSCFGEISILNKGSKGNRTANIRSL 545
Db 378 KGDIGREMYIIREGQAVAVDDGVTQYAVLGLYFGEISIIINIKGNSGNRTANIKSL 437
QY 546 GYSDFCLSKDDLEAVEAPDAKKVLEERGRILLMKWGLLDENEVAASMEVDVQV- 601

Db 438 GYSDFCLSKEDLREVLSEYPOAQVMEKRGREILLKMKLDVNAEAA--ETALQEAES 495
QY 602 KLEQLETNMDTLYTRFARLLAEYTGAAQKLKQRIIVLETKMKQNHEDDYLSDGINTPEP 660
Db 496 RUKGJQDDLDLQTRFARLLAELESSALKIAYIRERLEWQTRWPMPEMDGEADDEAP 554
RESULT 15
S52072
DmCNGC protein - fruit fly (Drosophila sp.)
C:Species: Drosophila sp.
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 16-Jul-1999
C:Accession: S52072
R:Baumann, A.; Frings, S.; Godde, M.; Seifert, R.; Kaupp, U.B.
EMBO J. 13, 5040-5050, 1994
A:Title: Primary structure and functional expression of a Drosophila cyclic nucleotide-
A:Reference number: S52072; MUID:95045396; PMID:7957070
A:Accession: S52072
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-665 <BAU>
C:Genetics:
A:Gene: FlyBase:Cng
A:Cross-references: FlyBase:FBgn0014462
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
F:429-553/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
Query Match 42.8%; Score 1487; DB 2; Length 665;
Best Local Similarity 52.3%; Pred. No. 9.9e-97;
Matches 299; Conservative 83; Mismatches 164; Indels 26; Gaps 6;
QY 87 REEPRPDSFLERFRGPELQTVTTHQGDGK- - - - -KDGEKGKTKKPFELVLDPA 138
Db 50 RNRKPPDPWFLEKFSN- - - - -TTNTDKIRKCPAMEDAALSSEIRGSSVLCNRLSVDP 103
QY 139 GMYRWLFVAMPVLYNWCLLVARACFSDLQRYFVWLVLDYFSDTVIADLIIRLT 198
Db 104 LOSHYRWLAIVSLAVLYNIIFVVGRAVFEINKSAPAFWYTLDCDFIYLLDTLVHME 163
QY 199 GFLEQGLLVKDPKKLRDNYHTLQKLDVASIIPDLYF- - - - -AVGIHSP- - - - -EVR 249
Db 164 GFLEQGLLVKDPKKLRDNYHTLQKLDVASIIPDLYF- - - - -AVGIHSP- - - - -EVR 249
QY 250 NELLHFAEFDFDRTETSTYFNIRISNLVLYILVLIHWNACIYVVISKSGIFGVD 309
Db 224 NELLRLNRFVLRPFEAFDRTEATAYENAPRIAKMLIYFVVIHWNACIYVVISKSGIFG 283
QY 310 VTPNTDPEYGLAREYIYCLWSTLTITIGETPPVKDEBYLFVIFDPLGLVLI 369
Db 284 VY- - - - -NLNGTRNNLTQRYISFYWSTLTITIGETTPENDVBYLFVADFLAGVLIFATI 342
QY 370 VGNVSGSMINMNATRAEFOAKIDAVKHVMQFRKVKSDMEAKVIKWFVLYLWTKTKV 429
Db 343 VGNISGSMINMNARVARFQNRMDGVQYMAFRVGHLEARVIRWFATYWSQSGALDE 402
QY 430 VLKNPAPKARAEIAINVHLSLTKKVRIFODWBAGLLVEILKLRPQVFSFGYICR 489
Db 403 VLAALPDKLKABIAIQVHMDTLKQVRIFPHDTPEGLLEALVLKLVQVSPGYICR 462
QY 490 GKEMYLIIKEGLAVAVDDGVTQYALLSAGSCFGEISILNKGSKGNRTANIRSL 549
Db 463 GKEMIVIRKGLSVVGGDGTITVLTGAGSVFGEVLEIAGNRTGNRTANIRSL 522
QY 550 LFCLSKDDLEAVEAPDAKKVLEERGRILLMKWGLLDENEVAASMEV- - - - -DVQEKLEQ 607
Db 523 LFCLAKRLDNLWLSYDPEARSLTQRCOLLKQKGLDLEQITFADSORVHDSIEGGIEK 582
QY 608 TNDTLYTRFARLLAEYTGAAQKLKQRIITVLE 639
Db 583 LSVENILNRLAEYTAQAKIKQLAKLE 614
Search completed: May 12, 2004, 11:15:45

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 12, 2004, 11:07:14 ; Search time 60 Seconds
(without alignments)
3126.859 Million cell updates/sec

Title: US-10-087-217A-8

Perfect score: 3475

Sequence: 1 MWTEKSNVGVKSPANNHH.....NHEDDYLSDGINTPEPTAAE 664

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 23Jan04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3475	100.0	664	6	Aae37222 Rat CNG c
2	3469	99.8	664	6	Aae37221 Rat CNG c
3	3456	99.5	664	6	Aae37224 Rat CNG c
4	3455	99.4	664	6	Aae37220 Rat CNG c
5	3455	99.4	664	6	Aae37223 Rat CNG c
6	3449	99.3	664	5	Aag79529 Rat HBMYC
7	3449	99.3	664	6	Aae37219 Rat CNG c
8	3384	97.4	664	5	Aag79528 Mouse HB
9	3231.5	93.0	732	5	Aag79526 Rabbit HB
10	3204.5	92.2	663	5	Aag79527 Cow HBMYC
11	3204.5	92.2	663	6	Abg74912 Bovine CN
12	3199.5	92.1	663	6	Abg74914 Bovine CN
13	3198.5	92.0	663	6	Abg74913 Bovine CN
14	3197.5	92.0	664	4	Aae04894 Human tra
15	3197.5	92.0	664	5	Abb78066 Amino aci
16	3197.5	92.0	664	6	Abg72530 Novel hum
17	3197.5	92.0	664	6	Abg72529 Novel hum
18	3197.5	92.0	664	6	Abu12049 Human NOV
19	3197.5	92.0	664	6	Abp98475 Amino aci
20	3184.5	91.6	664	5	Aag79525 Variant H
21	3179.5	91.5	664	5	Aag79524 HBMYCNG.
22	2139	61.6	694	5	Aae15987 Human CNG
23	2139	61.6	694	7	Aae38591 Human CNG
24	2034	58.5	686	7	Add48640 Human Pro
25	2030	58.4	690	7	Add93244 Cyclic nu

26	2028	58.4	690	5	AAE15988	AAE15988 Human CNG
27	2026	58.3	683	7	ADD48638	ADD48638 Rat Prote
28	1545	44.5	575	5	ABP69252	ABP69252 Human pol
29	1545	44.5	575	5	AAE20959	AAE20959 Human tra
30	1545	44.5	575	5	ABU07725	ABU07725 Human cyc
31	1545	44.5	575	6	ABU09091	ABU09091 Human tra
32	1545	44.5	575	6	ABP55141	ABP55141 Human cyc
33	1544	44.4	568	6	ABP55142	ABP55142 Human cyc
34	1543	44.4	575	6	ABU09778	ABU09778 Human tra
35	1540	44.3	575	5	AAO14138	AAO14138 Human tra
36	1540	44.3	575	5	AAW47673	AAW47673 MOL10b pr
37	1529	44.0	578	5	AAW47672	AAW47672 MOL10a pr
38	1494	43.0	665	4	ABB63493	ABB63493 Drosophil
39	1185	34.1	239	6	ABP98582	ABP98582 Amino aci
40	1166	33.6	239	6	ABR39397	ABR39397 Amino aci
41	1129	32.5	702	4	ABH65859	ABH65859 Drosophil
42	1057.5	30.4	1704	6	ABU09092	ABU09092 Rat trans
43	989.5	28.5	1693	4	ABB64282	ABB64282 Drosophil
44	870.5	25.1	1037	4	ABB66545	ABB66545 Drosophil
45	825	23.7	259	4	ABG27071	ABG27071 Novel hum

ALIGNMENTS

RESULT 1

AAE37222
ID AAE37222 standard; protein; 664 AA.

XX AAE37222;

DT 07-AUG-2003 (first entry)

DE Rat CNG channel alpha subunit mutant (C460W-Y565A-E583W).

XX Rat; G protein-coupled receptor; cyclic nucleotide-gated channel; GPCR;
cyclic nucleotide-gated channel; CNG channel; mutant; mutuin.

OS Rattus norvegicus.

OS Synthetic.

FX Key Location/Qualifiers

FT Misc-difference 460

FT /note= "Wild type Cys substituted with Trp"

FT Misc-difference 565

FT /note= "Wild type Tyr substituted with Ala"

FT Misc-difference 583

FT /note= "Wild type Glu substituted with Met"

XX WO2003038039-A2.

XX 08-MAY-2003.

XX 25-OCT-2002; 2002WO-US034122.

XX 26-OCT-2001; 2001US-0330663P.

XX 04-MAR-2002; 2002US-00087217.

XX (APTU-) APTUS PHARM INC.

XX Yao Y, Cao L;

XX WPI; 2003-430510/40.

XX N-PSDB; AAD56242.

XX New host cell comprising first and second nucleic acids with promoters
that encode exogenous G protein-coupled receptor and cyclic nucleotide-
gated channel, respectively, useful for identifying agents that modulate
GPCR activity.

XX Claim 13; Page 95-98; 98pp; English.

XX The invention relates to compositions and methods for identifying G

CC protein-coupled receptor (GPCR), ligands and compounds that modulate GPCR
 CC -mediated activities. The invention also provides an host cell comprising
 CC first and second nucleic acids with promoters that encode exogenous G
 CC protein-coupled receptor and cyclic nucleotide-gated (CNG) channel
 CC respectively. The host cells are useful for identifying agents that
 CC modulate an activity mediated by a GPCR. The present sequence is rat CNG
 CC channel alpha subunit mutant
 XX
 SQ Sequence 664 AA;

Query Match 100.0%; Score 3475; DB 6; Length 664;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 664; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEKSGVKSSPANNHHPPSIKANGKDDHAGSRPQSVAAADDTSPQLRLAEMDT 60
 DB 1 MTEKSGVKSSPANNHHPPSIKANGKDDHAGSRPQSVAAADDTSPQLRLAEMDT 60
 QY 61 PRGRGGFQRIIVRLVGIVRDWANKNFRPEPRDPSFLERFRGPPELQTVTHQDDKGGKD 120
 DB 61 PRGRGGFQRIIVRLVGIVRDWANKNFRPEPRDPSFLERFRGPPELQTVTHQDDKGGKD 120
 QY 121 GEGKGTKKKPELVLDPPAGDWYRMLFVIAMPVLYNWCLLVARACFSDLQRYFVWLV 180
 DB 121 GEGKGTKKKPELVLDPPAGDWYRMLFVIAMPVLYNWCLLVARACFSDLQRYFVWLV 180
 QY 181 DYFSDTVYIADLIIRLTGFLQGLLVKDPKRLDNVYIHTLQKLDVASIITPTDLYFAV 240
 DB 181 DYFSDTVYIADLIIRLTGFLQGLLVKDPKRLDNVYIHTLQKLDVASIITPTDLYFAV 240
 QY 241 GIHSPEVRNRLHFAFMPEFFDRTETRTSYNIFRISNLVLYIHNACIYVVISK 300
 DB 241 GIHSPEVRNRLHFAFMPEFFDRTETRTSYNIFRISNLVLYIHNACIYVVISK 300
 QY 301 SIGFGVDTWVYNIITDPEGYLAREYIYCLYWSLTILTTIGETPPPVKDEEYLFVIFDEL 360
 DB 301 SIGFGVDTWVYNIITDPEGYLAREYIYCLYWSLTILTTIGETPPPVKDEEYLFVIFDEL 360
 QY 361 IGVLIFATIVGNVGMISNNMTRAEFAKIDAVKHYMQFRKYSKDMEAKVIKWFYDLWT 420
 DB 361 IGVLIFATIVGNVGMISNNMTRAEFAKIDAVKHYMQFRKYSKDMEAKVIKWFYDLWT 420
 QY 421 NKKTVDEREVLKMLPAKLAIEAIVNHLSTLTKKVRIFQDWEAGLLVELVLKLPQVFSFG 480
 DB 421 NKKTVDEREVLKMLPAKLAIEAIVNHLSTLTKKVRIFQDWEAGLLVELVLKLPQVFSFG 480
 QY 481 DYICRKGDIKEMWIIKEGKLAVADDGVTOYALLSAGSCFGEISIIINIKSGKGNRRTA 540
 DB 481 DYICRKGDIKEMWIIKEGKLAVADDGVTOYALLSAGSCFGEISIIINIKSGKGNRRTA 540
 QY 541 NIRSGLVSDLCFSLSKDLMFAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQ 600
 DB 541 NIRSGLVSDLCFSLSKDLMFAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQ 600
 QY 601 EKLEQETNMDITYRPARLLAETGAQOKLKRITVLETMKQNHDDYLSGINTPEP 660
 DB 601 EKLEQETNMDITYRPARLLAETGAQOKLKRITVLETMKQNHDDYLSGINTPEP 660
 QY 661 TAAE 664
 DB 661 TAAE 664

RESULT 2

AAE37221

ID AAE37221 standard; protein; 664 AA.

XX

AC AAE37221;

XX

DT 07-AUG-2003 (first entry)

XX

DE Rat CNG channel alpha subunit mutant.

XX

KW Rat; G protein-coupled receptor; cyclic nucleotide-gated channel; GPCR;
 KW cyclic nucleotide-gated channel; CNG channel; mutant; mutein.

OS Rattus norvegicus.
 OS Synthetic.

PN WO2003038039-A2.

XX 08-MAY-2003.

XX 25-OCT-2002; 2002WO-US034122.

XX 26-OCT-2001; 2001US-0330663P.

PR 04-MAR-2002; 2002US-00087217.

XX (AFTU-) APTUS PHARM INC.

PI Yao Y, Cao L;

DR WPI; 2003-430510/40.

DR N-PSDB; AAD56241.

XX New host cell comprising first and second nucleic acids with promoters
 PT that encode exogenous G protein-coupled receptor and cyclic nucleotide-
 PT gated channel, respectively, useful for identifying agents that modulate
 PT GPCR activity.

PS Claim 13; Page 89-92; 98pp; English.

XX The invention relates to compositions and methods for identifying G
 CC protein-coupled receptor (GPCR), ligands and compounds that modulate GPCR
 CC -mediated activities. The invention also provides an host cell comprising
 CC first and second nucleic acids with promoters that encode exogenous G
 CC protein-coupled receptor and cyclic nucleotide-gated (CNG) channel
 CC respectively. The host cells are useful for identifying agents that
 CC modulate an activity mediated by a GPCR. The present sequence is rat CNG
 CC channel alpha subunit mutant

XX Sequence 664 AA;

Query Match 99.8%; Score 3469; DB 6; Length 664;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 663; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTEKSGVKSSPANNHHPPSIKANGKDDHAGSRPQSVAAADDTSPQLRLAEMDT 60
 DB 1 MTEKSGVKSSPANNHHPPSIKANGKDDHAGSRPQSVAAADDTSPQLRLAEMDT 60
 QY 61 PRGRGGFQRIIVRLVGIVRDWANKNFRPEPRDPSFLERFRGPPELQTVTHQDDKGGKD 120
 DB 61 PRGRGGFQRIIVRLVGIVRDWANKNFRPEPRDPSFLERFRGPPELQTVTHQDDKGGKD 120
 QY 121 GEGKGTKKKPELVLDPPAGDWYRMLFVIAMPVLYNWCLLVARACFSDLQRYFVWLV 180
 DB 121 GEGKGTKKKPELVLDPPAGDWYRMLFVIAMPVLYNWCLLVARACFSDLQRYFVWLV 180
 QY 181 DYFSDTVYIADLIIRLTGFLQGLLVKDPKRLDNVYIHTLQKLDVASIITPTDLYFAV 240
 DB 181 DYFSDTVYIADLIIRLTGFLQGLLVKDPKRLDNVYIHTLQKLDVASIITPTDLYFAV 240
 QY 241 GIHSPEVRNRLHFAFMPEFFDRTETRTSYNIFRISNLVLYIHNACIYVVISK 300
 DB 241 GIHSPEVRNRLHFAFMPEFFDRTETRTSYNIFRISNLVLYIHNACIYVVISK 300
 QY 301 SIGFGVDTWVYNIITDPEGYLAREYIYCLYWSLTILTTIGETPPPVKDEEYLFVIFDEL 360
 DB 301 SIGFGVDTWVYNIITDPEGYLAREYIYCLYWSLTILTTIGETPPPVKDEEYLFVIFDEL 360
 QY 361 IGVLIFATIVGNVGMISNNMTRAEFAKIDAVKHYMQFRKYSKDMEAKVIKWFYDLWT 420
 DB 361 IGVLIFATIVGNVGMISNNMTRAEFAKIDAVKHYMQFRKYSKDMEAKVIKWFYDLWT 420
 QY 421 NKKTVDEREVLKMLPAKLAIEAIVNHLSTLTKKVRIFQDWEAGLLVELVLKLPQVFSFG 480

```

Db 421 NKKTVDEREVLKPKLPAKRAEIAINVHLSTLKKVRFQDWEAGLLVELVLRPQVFSFG 480
QY 481 DYICRKGDIKEMYYIKKGLAVVADGGVTVALLSAGSCFGEISILNKGKMGNRRTA 540
Db 481 DYICRKGDIKEMYYIKKGLAVVADGGVTVALLSAGSCFGEISILNKGKMGNRRTA 540
QY 541 NIRSGLYDLFCLSKDDLMFAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQ 600
Db 541 NIRSGLYDLFCLSKDDLMFAVTEYDPAKKVLEERGREILMKMGLLDENEVAASMEVDVQ 600
QY 601 EKLEQLETNMDLTLYTRFARLLAAYTGAQOKLKORIIVLETMKMKQNHEDDYLSDGINTPEP 660
Db 601 EKLEQLETNMDLTLYTRFARLLAAYTGAQOKLKORIIVLETMKMKQNHEDDYLSDGINTPEP 660
QY 661 TAAE 664
Db 661 TAAE 664

RESULT 3
AAE37224
ID AAE37224 standard; protein; 664 AA.
XX
AC AAE37224;
XX
XX 07-AUG-2003 (first entry)
XX
DE Rat CNG channel alpha subunit mutant (C460H+E583W).
XX
XX Rat; G protein-coupled receptor; cyclic nucleotide-gated channel; GPCR;
KW cyclic nucleotide-gated channel; CNG channel; mutant; mutein.
XX
XX Rattus norvegicus.
OS
OS Synthetic.
FH Key Location/Qualifiers
FT Misc-difference 460
FT /note= "Wild type Cys substituted with His"
FT Misc-difference 583
FT /note= "Wild type Glu substituted with Met"
XX
XX WO2003038039-A2.
XX
XX 08-MAY-2003.
XX
XX 25-OCT-2002; 2002WO-US034122.
XX
XX 26-OCT-2001; 2001US-0330663P.
XX
XX 04-MAR-2002; 2002US-00087217.
XX
XX (APTU-) APTUS PHARM INC.
XX
XX Yao Y, Cao L;
XX
XX WPI; 2003-430510/40.
XX
XX New host cell comprising first and second nucleic acids with promoters.
PT that encode exogenous G protein-coupled receptor and cyclic nucleotide-
PT gated channel, respectively, useful for identifying agents that modulate
PT GPCR activity.
XX
XX Example 10; Page; 98pp; English.
XX
XX The invention relates to compositions and methods for identifying G
XX protein-coupled receptor (GPCR), ligands and compounds that modulate GPCR
XX mediated activities. The invention also provides an host cell comprising
XX first and second nucleic acids with promoters that encode exogenous G
XX protein-coupled receptor and cyclic nucleotide-gated (CNG) channel
XX respectively. The host cells are useful for identifying agents that
XX modulate an activity mediated by a GPCR. The present sequence is rat CNG
XX channel alpha subunit mutant. Note: This sequence is not shown in the
XX specification but is derived from the rat CNG channel alpha subunit wild-

```

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CC type protein shown as SEQ ID NO: 2 (AAE37219) in page 78-80 of the
CC specification
XX
SQ Sequence 664 AA;
Query Match 99.5%; Score 3456; DB 6; Length 664;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 662; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MMTESKNGVKSPANNHHPPPSIKANKGDHRRAGSRPQSVAAADDTSPELQRLAEMDT 60
Db 1 MMTESKNGVKSPANNHHPPPSIKANKGDHRRAGSRPQSVAAADDTSPELQRLAEMDT 60
QY 61 PRGRGGGFQRIIVRLGVIRDMANKFRREPEEPDPSFLERFRGPELQTVTTHQDDKGGKD 120
Db 61 PRGRGGGFQRIIVRLGVIRDMANKFRREPEEPDPSFLERFRGPELQTVTTHQDDKGGKD 120
QY 121 GEGKGTKKKFELFVLDPAGDWTYRWLFVIAMPVLYNWCILVARACFSDLQRNYFVWVLVL 180
Db 121 GEGKGTKKKFELFVLDPAGDWTYRWLFVIAMPVLYNWCILVARACFSDLQRNYFVWVLVL 180
QY 181 DYFSDTVIADLIIRLTGFLGQLLVKDPKKLRDNYIHTLQFKLDVASIIPDLYFAV 240
Db 181 DYFSDTVIADLIIRLTGFLGQLLVKDPKKLRDNYIHTLQFKLDVASIIPDLYFAV 240
QY 241 GIHSPEVRENLLHFARMEFEFDRTESTRSYNIFRISNLVLYLIIHWNACIYVVISK 300
Db 241 GIHSPEVRENLLHFARMEFEFDRTESTRSYNIFRISNLVLYLIIHWNACIYVVISK 300
QY 301 SIGFGVDTWVYNIITDPEYGLAREYIYCLYKSTLTLTIGETPPVKDEEYLFVIFDEL 360
Db 301 SIGFGVDTWVYNIITDPEYGLAREYIYCLYKSTLTLTIGETPPVKDEEYLFVIFDEL 360
QY 361 IGVLIIFATIVGNVSMISNMNATRAEFQAKIDAVKHVMQFRKVSQDMBAKVIKWFYLT 420
Db 361 IGVLIIFATIVGNVSMISNMNATRAEFQAKIDAVKHVMQFRKVSQDMBAKVIKWFYLT 420
QY 421 NKKTVDEREVLKPKLPAKRAEIAINVHLSTLKKVRFQDWEAGLLVELVLRPQVFSFG 480
Db 421 NKKTVDEREVLKPKLPAKRAEIAINVHLSTLKKVRFQDWEAGLLVELVLRPQVFSFG 480
QY 481 DYICRKGDIKEMYYIKKGLAVVADGGVTVALLSAGSCFGEISILNKGKMGNRRTA 540
Db 481 DYICRKGDIKEMYYIKKGLAVVADGGVTVALLSAGSCFGEISILNKGKMGNRRTA 540
QY 541 NIRSGLYDLFCLSKDDLMFAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQ 600
Db 541 NIRSGLYDLFCLSKDDLMFAVTEYDPAKKVLEERGREILMKMGLLDENEVAASMEVDVQ 600
QY 601 EKLEQLETNMDLTLYTRFARLLAAYTGAQOKLKORIIVLETMKMKQNHEDDYLSDGINTPEP 660
Db 601 EKLEQLETNMDLTLYTRFARLLAAYTGAQOKLKORIIVLETMKMKQNHEDDYLSDGINTPEP 660
QY 661 TAAE 664
Db 661 TAAE 664

RESULT 4
AAE37220
ID AAE37220 standard; protein; 664 AA.
XX
XX AAE37220;
XX
XX 07-AUG-2003 (first entry)
XX
XX Rat CNG channel alpha subunit mutant (Y565A).
XX
XX Rat; G protein-coupled receptor; cyclic nucleotide-gated channel; GPCR;
KW cyclic nucleotide-gated channel; CNG channel; mutant; mutein.
XX
XX Rattus norvegicus.
OS
OS Synthetic.

```

XX Key Location/Qualifiers
 FH Misc-difference 565 /note= "Wild type Tyr substituted with Ala"
 FT
 XX
 XX W02003038039-A2.
 XX
 XX 08-MAY-2003.
 XX
 XX 25-OCT-2002; 2002WO-US034122.
 XX
 XX 26-OCT-2001; 2001US-0330663P.
 PR
 PR 04-MAR-2002; 2002US-00087217.
 XX
 XX (APTU-) APTUS PHARM INC.
 XX
 XX Yao Y, Cao L;
 XX
 DR WPI; 2003-430510/40.
 DR N-PSDB; AAD56240.
 XX
 XX New host cell comprising first and second nucleic acids with promoters
 PT that encode exogenous G protein-coupled receptor and cyclic nucleotide-
 PT gated channel, respectively, useful for identifying agents that modulate
 PT GPCR activity.
 XX
 XX Claim 13; Page 84-86; 98pp; English.
 XX
 XX The invention relates to compositions and methods for identifying G
 CC protein-coupled receptor (GPCR), ligands and compounds that modulate GPCR
 CC mediated activities. The invention also provides an host cell comprising
 CC first and second nucleic acids with promoters that encode exogenous G
 CC protein-coupled receptor and cyclic nucleotide-gated (CNG) channel
 CC respectively. The host cells are useful for identifying agents that
 CC modulate an activity mediated by a GPCR. The present sequence is rat CNG
 CC channel alpha subunit mutant
 XX
 SQ Sequence 664 AA;
 Query Match 99.4%; Score 3455; DB 6; Length 664;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 662; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MMTKSNVGVKSSPANNHPPPSIKANGKDDHRRAGSRPQSVAAADDDTSPQLQRLAEMDT 60
 DB 1 MMTKSNVGVKSSPANNHPPPSIKANGKDDHRRAGSRPQSVAAADDDTSPQLQRLAEMDT 60
 QY 61 PRGRGGFQRIVLVGVIRDWANKNFRPEEPDPSFLERPRGPPELQVTTTHQGDGKGD 120
 DB 61 PRGRGGFQRIVLVGVIRDWANKNFRPEEPDPSFLERPRGPPELQVTTTHQGDGKGD 120
 QY 121 GEGGKTKKKEFLVLDPAQDWYRWLFVIAIMPVLYNWCILVARACTSDLQRYFVWLV 180
 DB 121 GEGGKTKKKEFLVLDPAQDWYRWLFVIAIMPVLYNWCILVARACTSDLQRYFVWLV 180
 QY 181 DYSFDTVYIADLIIRLTGTELEQGLVKDPKRLDNYIHTLQFKLDVASIPTDLIYFV 240
 DB 181 DYSFDTVYIADLIIRLTGTELEQGLVKDPKRLDNYIHTLQFKLDVASIPTDLIYFV 240
 QY 241 GIHSPEVRNELLHFAHMPFFEDTETRTSYNPIFRISNLVILVILHWNACIYYVISK 300
 DB 241 GIHSPEVRNELLHFAHMPFFEDTETRTSYNPIFRISNLVILVILHWNACIYYVISK 300
 QY 301 SIGFGVDTWYPNITDEYGLAREYIYCLYWSLTITLTIGETPPPVKDEYLFVDPFL 360
 DB 301 SIGFGVDTWYPNITDEYGLAREYIYCLYWSLTITLTIGETPPPVKDEYLFVDPFL 360
 QY 361 IGVLIPTATVGNVSMISNNNATRAEFQAKIDAVKHYMQFRKYSKDMKAEKVIKWFYLT 420
 DB 361 IGVLIPTATVGNVSMISNNNATRAEFQAKIDAVKHYMQFRKYSKDMKAEKVIKWFYLT 420
 QY 421 NKKTVDREVLKXNPAKLRRAEIAINVHLSLTKKVRIFQDCEAGLLVVLKLRPQVPSFG 480

DB 421 NKKTVDREVLKXNPAKLRRAEIAINVHLSLTKKVRIFQDCEAGLLVVLKLRPQVPSFG 480
 QY 481 DYTCKRGDICKENYIIKEGKLAVADDGVTQVALLSAGSCFGGSEISILINIKSGKMGNRRTA 540
 DB 481 DYTCKRGDICKENYIIKEGKLAVADDGVTQVALLSAGSCFGGSEISILINIKSGKMGNRRTA 540
 QY 541 NIRSIGVSDLFCLSKDDLMFAVTEAPDAKKVLEERGREIILMKMGLLDENEVAASMEVDVQ 600
 DB 541 NIRSIGVSDLFCLSKDDLMFAVTEAPDAKKVLEERGREIILMKMGLLDENEVAASMEVDVQ 600
 QY 601 EKLEQLETNMDTLYTRFARLLAEYTGAAQOKLQRIITVLETKMKQKHEDDYLSGINTPEP 660
 DB 601 EKLEQLETNMDTLYTRFARLLAEYTGAAQOKLQRIITVLETKMKQKHEDDYLSGINTPEP 660
 QY 661 TAAE 664
 DB 661 TAAE 664
 RESULT 5
 AAE37223
 ID AAE37223 standard; protein; 664 AA.
 XX
 AC AAE37223;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE Rat CNG channel alpha subunit mutant (C460R+E583M).
 XX
 KW Rat; G protein-coupled receptor; cyclic nucleotide-gated channel; GPCR;
 KW cyclic nucleotide-gated channel; CNG channel; mutant; mutein.
 XX
 OS Rattus norvegicus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 460 /note= "Wild type Cys substituted with Arg"
 FT
 FT Misc-difference 593 /note= "Wild type Glu substituted with Met"
 XX
 FN W02003038039-A2.
 XX
 XX 08-MAY-2003.
 XX
 XX 25-OCT-2002; 2002WO-US034122.
 XX
 XX 26-OCT-2001; 2001US-0330663P.
 PR
 PR 04-MAR-2002; 2002US-00087217.
 XX
 XX (APTU-) APTUS PHARM INC.
 XX
 XX Yao Y, Cao L;
 XX
 XX WPI; 2003-430510/40.
 XX
 XX New host cell comprising first and second nucleic acids with promoters
 PT that encode exogenous G protein-coupled receptor and cyclic nucleotide-
 PT gated channel, respectively, useful for identifying agents that modulate
 PT GPCR activity.
 XX
 XX Example 10; Page; 98pp; English.
 XX
 XX The invention relates to compositions and methods for identifying G
 CC protein-coupled receptor (GPCR), ligands and compounds that modulate GPCR
 CC mediated activities. The invention also provides an host cell comprising
 CC first and second nucleic acids with promoters that encode exogenous G
 CC protein-coupled receptor and cyclic nucleotide-gated (CNG) channel
 CC respectively. The host cells are useful for identifying agents that
 CC modulate an activity mediated by a GPCR. The present sequence is rat CNG
 CC channel alpha subunit mutant. Note: This sequence is not shown in the
 CC specification but is derived from the rat CNG channel alpha subunit wild-
 CC type protein shown as SEQ ID NO: 2 (AAE37219) in page 78-80 of the

```

CC specification
XX SQ Sequence 664 AA;
    Query Match      99.4%; Score 3455; DB 6; Length 664;
    Best Local Similarity 99.7%; Pred. No. 0;
    Matches 662; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MMTEKSGVGVSSPANNHHPPPSIKANGKDDHRAGSRPOSVAADDDTSPQLRLAEMDT 60
Db 1 MMTEKSGVGVSSPANNHHPPPSIKANGKDDHRAGSRPOSVAADDDTSPQLRLAEMDT 60
QY 61 PRGRGGFQRIVLGVIRDMWANKNPREPRDPSFLERPRGPELQTVTHQGDGKGD 120
Db 61 PRGRGGFQRIVLGVIRDMWANKNPREPRDPSFLERPRGPELQTVTHQGDGKGD 120
QY 121 GEGKGTKKKFEFLVDPAGDWYRWLFVIAIMPVLVNWCLLVARACFSDLQRYFVWLV 180
Db 121 GEGKGTKKKFEFLVDPAGDWYRWLFVIAIMPVLVNWCLLVARACFSDLQRYFVWLV 180
QY 181 DYFSDTVYIADLIIRLTGFLQGLLVKPKLRDNYIHTLQPKLDVASIIPDLYFV 240
Db 181 DYFSDTVYIADLIIRLTGFLQGLLVKPKLRDNYIHTLQPKLDVASIIPDLYFV 240
QY 241 GIHSPVRENRLLHFARMFEFFDRTETRTSYPNIFRISNLVILVILVHWNACIYV 300
Db 241 GIHSPVRENRLLHFARMFEFFDRTETRTSYPNIFRISNLVILVILVHWNACIYV 300
QY 301 SIGFGVDTWVYPNITDPEYGLAREYIYCLYNWSTLTITIGETPPPVKDEYLFV 360
Db 301 SIGFGVDTWVYPNITDPEYGLAREYIYCLYNWSTLTITIGETPPPVKDEYLFV 360
QY 361 IGVLIFATIVGVNVSIMNNATRAEFQAKIDAVKHVMQFRKYSKOMEAKVIKWF 420
Db 361 IGVLIFATIVGVNVSIMNNATRAEFQAKIDAVKHVMQFRKYSKOMEAKVIKWF 420
QY 421 NKKTVDEREVLKMLPAKLRAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKRP 480
Db 421 NKKTVDEREVLKMLPAKLRAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKRP 480
QY 481 DYICRKGDIKEMYYIIKEGKLVAVDDGVTQYALLSAGSCFGEISILNKGKGN 540
Db 481 DYICRKGDIKEMYYIIKEGKLVAVDDGVTQYALLSAGSCFGEISILNKGKGN 540
QY 541 NIRSGLVSDLCFCLSKODLMEAVTEAPAKVLEERGREIILMKGLLDENEVAAS 600
Db 541 NIRSGLVSDLCFCLSKODLMEAVTEAPAKVLEERGREIILMKGLLDENEVAAS 600
QY 601 EKLEQLETNMDTLYTRFARLLAETGAQOKIKORITVLETKMKONHEDDYLSD 660
Db 601 EKLEQLETNMDTLYTRFARLLAETGAQOKIKORITVLETKMKONHEDDYLSD 660
QY 661 TAAB 664
Db 661 TAAB 664
RESULT 6
AAG79529
ID AAG79529 standard; protein; 664 AA.
XX AC AAG79529;
XX DT 09-DEC-2002 (first entry)
XX DE Rat HBMVCNG.
XX KW Human; cation channel; cyclic nucleotide gated; HBMVCNG;
XX KW ion channel-related disorder; stroke; depression; liver disease;
XX KW Alzheimer's disease; Parkinson's disease; arrhythmia; diabetes;
XX KW chronic pain; hypercalcaemia; hypocalcaemia; hypercalciuria; anxiety;
XX KW hypocalciuria; gastrointestinal disorder; renal disease.

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OS Rattus norvegicus.
XX PN WC200268471-A2.
XX PD 06-SEP-2002.
XX PF 21-DEC-2001; 2001WO-US050413.
XX PR 21-DEC-2000; 2000US-0257865P.
XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX PI Feder J, Mintier G, Ramanathan C, Westphal R;
XX DR WPI; 2002-691655/74.
XX PT New human HBMVCNG genes, useful for treating ion channel-related
XX PT disorders e.g. stroke, anxiety and depression, Alzheimer's or Parkinson's
XX PT disease, diabetes or arrhythmia.
XX PS Disclosure; Fig 4; 177pp; English.
XX CC The sequences given in AAG79526-29 represent rabbit, cow, mouse and rat
XX CC versions of the human cation channel polypeptide designated HBMVCNG.
XX CC HBMVCNG is a human cyclic nucleotide gated cation channel with six
XX CC transmembrane domains. HBMVCNG genes are useful for treating ion channel-
XX CC related disorders, e.g. stroke, anxiety and depression, Alzheimer's or
XX CC Parkinson's disease, arrhythmia, diabetes, chronic pain, hypercalcaemia,
XX CC hypocalcaemia, hypercalciuria, hypocalciuria, gastrointestinal disorders,
XX CC ion disorders or renal or liver disease
XX SQ Sequence 664 AA;
    Query Match      99.3%; Score 3449; DB 5; Length 664;
    Best Local Similarity 99.5%; Pred. No. 0;
    Matches 661; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MMTEKSGVGVSSPANNHHPPPSIKANGKDDHRAGSRPOSVAADDDTSPQLRLAEMDT 60
Db 1 MMTEKSGVGVSSPANNHHPPPSIKANGKDDHRAGSRPOSVAADDDTSPQLRLAEMDT 60
QY 61 PRGRGGFQRIVLGVIRDMWANKNPREPRDPSFLERPRGPELQTVTHQGDGKGD 120
Db 61 PRGRGGFQRIVLGVIRDMWANKNPREPRDPSFLERPRGPELQTVTHQGDGKGD 120
QY 121 GEGKGTKKKFEFLVDPAGDWYRWLFVIAIMPVLVNWCLLVARACFSDLQRYFVWLV 180
Db 121 GEGKGTKKKFEFLVDPAGDWYRWLFVIAIMPVLVNWCLLVARACFSDLQRYFVWLV 180
QY 181 DYFSDTVYIADLIIRLTGFLQGLLVKPKLRDNYIHTLQPKLDVASIIPDLYFV 240
Db 181 DYFSDTVYIADLIIRLTGFLQGLLVKPKLRDNYIHTLQPKLDVASIIPDLYFV 240
QY 241 GIHSPVRENRLLHFARMFEFFDRTETRTSYPNIFRISNLVILVILVHWNACIYV 300
Db 241 GIHSPVRENRLLHFARMFEFFDRTETRTSYPNIFRISNLVILVILVHWNACIYV 300
QY 301 SIGFGVDTWVYPNITDPEYGLAREYIYCLYNWSTLTITIGETPPPVKDEYLFV 360
Db 301 SIGFGVDTWVYPNITDPEYGLAREYIYCLYNWSTLTITIGETPPPVKDEYLFV 360
QY 361 IGVLIFATIVGVNVSIMNNATRAEFQAKIDAVKHVMQFRKYSKOMEAKVIKWF 420
Db 361 IGVLIFATIVGVNVSIMNNATRAEFQAKIDAVKHVMQFRKYSKOMEAKVIKWF 420
QY 421 NKKTVDEREVLKMLPAKLRAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKRP 480
Db 421 NKKTVDEREVLKMLPAKLRAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKRP 480
QY 481 DYICRKGDIKEMYYIIKEGKLVAVDDGVTQYALLSAGSCFGEISILNKGKGN 540
Db 481 DYICRKGDIKEMYYIIKEGKLVAVDDGVTQYALLSAGSCFGEISILNKGKGN 540

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QY 541 NIRSGLYSDLFCLSKODLMEAVTEAPDAKKVLEERGRIILMKGLLDENEVAASMEVDVQ 600
 DB 541 NIRSGLYSDLFCLSKODLMEAVTEYDPAKKVLEERGRIILMKGLLDENEVAASMEVDVQ 600
 QY 601 EKLEQLETNMDTLYTRFARLLAEVTGAQOKLQKRIITVLETKMKQNHEDDYLSDGINTPEP 660
 DB 601 EKLEQLETNMDTLYTRFARLLAEVTGAQOKLQKRIITVLETKMKQNHEDDYLSDGINTPEP 660
 QY 661 TAAE 664
 DB 661 TAAE 664

RESULT 7
 AAE37219
 ID AAE37219 standard; protein; 664 AA.
 XX
 AC AAE37219;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE Rat CNG channel alpha subunit wild-type protein.
 XX
 KW Rat; G protein-coupled receptor; cyclic nucleotide-gated channel; GPCR;
 KW cyclic nucleotide-gated channel; CNG channel.
 XX
 OS Rattus norvegicus.
 XX
 PN WO2003038039-A2.
 XX
 PD 08-MAY-2003.
 XX
 PF 25-OCT-2002; 2002WO-US034122.
 XX
 PR 26-OCT-2001; 2001US-0330663P.
 PR 04-MAR-2002; 2002US-00087217.
 XX
 PA (APTU-) APTUS PHARM INC.
 XX
 PI Yao Y, Cao L;
 XX
 DR WPI; 2003-430510/40.
 DR N-PSDB; AAD56239.
 XX
 PT New host cell comprising first and second nucleic acids with promoters
 PT that encode exogenous G protein-coupled receptor and cyclic nucleotide-
 PT gated channel, respectively, useful for identifying agents that modulate
 PT GPCR activity.
 XX
 PS Claim 13; Page 78-80; 98pp; English.
 XX
 CC The invention relates to compositions and methods for identifying G
 CC protein-coupled receptor (GPCR), ligands and compounds that modulate GPCR
 CC mediated activities. The invention also provides an host cell comprising
 CC first and second nucleic acids with promoters that encode exogenous G
 CC protein-coupled receptor and cyclic nucleotide-gated (CNG) channel
 CC respectively. The host cells are useful for identifying agents that
 CC modulate an activity mediated by a GPCR. The present sequence is rat CNG
 CC channel alpha subunit wild-type protein
 XX
 SQ Sequence 664 AA;

Query Match 99.3%; Score 3449; DB 6; Length 664;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 661; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MMTKSNVGVKSSPANNHHPPPSIKANGKDDHRAGRPSQVAADDOTSPLOQLAEMDT 60
 DB 1 MMTKSNVGVKSSPANNHHPPPSIKANGKDDHRAGRPSQVAADDOTSPLOQLAEMDT 60
 QY 61 PRRGGGGFORIVRLVGVIRWANKNFREERPRPDSFLERFRGPBLQVTTWHQGGDKGKD 120
 DB 61 PRRGGGGFORIVRLVGVIRWANKNFREERPRPDSFLERFRGPBLQVTTWHQGGDKGKD 120

RESULT 8

AAG79528

ID AAG79528 standard; protein; 664 AA.

XX

AC AAG79528;

XX

DT 03-DEC-2002 (first entry)

XX

DE Mouse HBMYCNG.

XX

KW Human; cation channel; cyclic nucleotide gated; HBMYCNG;
 KW ion channel-related disorder; stroke; depression; liver disease;
 KW Alzheimer's disease; Parkinson's disease; arrhythmia; diabetes;
 KW chronic pain; hypercalcaemia; hypocalcaemia; hypercalciuria; anxiety;
 KW hypocalciuria; gastrointestinal disorder; renal disease.

XX

OS Mus musculus.

XX

PN WO200268471-A2.

XX

PD 06-SEP-2002.

XX

PF 21-DEC-2001; 2001WO-US050413.

XX

PR 21-DEC-2000; 2000US-0257865P.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Feder J, Mintier G, Ramanathan C, Westphal R;

XX

DR WPI; 2002-691655/74.

121 GEGKTKKKFELFVLDPAGDWYRWFVLTAMPVLYNWCLLVARACFSDLQRNVFVWLVL 180
 DB 121 GEGKTKKKFELFVLDPAGDWYRWFVLTAMPVLYNWCLLVARACFSDLQRNVFVWLVL 180
 QY 181 DYPSTDVYIADLIIRLTGFLQGLLVKOPKKLRDNYIHTLQPKLDVASIIPTDLIYFV 240
 DB 181 DYPSTDVYIADLIIRLTGFLQGLLVKOPKKLRDNYIHTLQPKLDVASIIPTDLIYFV 240
 QY 241 GIHSPEVRNRLHFAFMFEFFDRTRTSYNIIFRISNLVLYIIVIHWNACIYVVISK 300
 DB 241 GIHSPEVRNRLHFAFMFEFFDRTRTSYNIIFRISNLVLYIIVIHWNACIYVVISK 300
 QY 301 SIGFGVDTWVYPNITDPEYGYLAREYIYCLYXWSTLTLTITGETPPPVKDBEYLVFLFDEL 360
 DB 301 SIGFGVDTWVYPNITDPEYGYLAREYIYCLYXWSTLTLTITGETPPPVKDBEYLVFLFDEL 360
 QY 361 IGVLIIPATIVGVNGVSMISNNATRAEFQAKIDAVKHVMQFRKYSKDMEAKVWKWFDYLT 420
 DB 361 IGVLIIPATIVGVNGVSMISNNATRAEFQAKIDAVKHVMQFRKYSKDMEAKVWKWFDYLT 420
 QY 421 NKKTVDEREVLKMLPAKLAETAINVHLSLTLLKKVRFQDWEAGLLVVELVILKRPQVSPG 480
 DB 421 NKKTVDEREVLKMLPAKLAETAINVHLSLTLLKKVRFQDWEAGLLVVELVILKRPQVSPG 480
 QY 481 DYICRKGDIGKEMYIIKEGKLAVVADGVTQYALLSAGSCFGEISILNKGSKWGNRRTA 540
 DB 481 DYICRKGDIGKEMYIIKEGKLAVVADGVTQYALLSAGSCFGEISILNKGSKWGNRRTA 540
 QY 541 NIRSGLYSDLFCLSKODLMEAVTEAPDAKKVLEERGRIILMKGLLDENEVAASMEVDVQ 600
 DB 541 NIRSGLYSDLFCLSKODLMEAVTEYDPAKKVLEERGRIILMKGLLDENEVAASMEVDVQ 600
 QY 601 EKLEQLETNMDTLYTRFARLLAEYTGAAQOKLQKRIITVLETKMKQNHEDDYLSDGINTPEP 660
 DB 601 EKLEQLETNMDTLYTRFARLLAEYTGAAQOKLQKRIITVLETKMKQNHEDDYLSDGINTPEP 660
 QY 661 TAAE 664
 DB 661 TAAE 664

XX New human HBMYCNG genes, useful for treating ion channel-related
PT disorders e.g. stroke, anxiety and depression, Alzheimer's or Parkinson's
PT disease, diabetes or arrhythmia.
XX
PS Disclosure; Fig 4; 177pp; English.
XX
CC The sequences given in AAG79526-29 represent rabbit, cow, mouse and rat
CC versions of the human cation channel polypeptide designated HBMYCNG.
CC HBMYCNG is a human cyclic nucleotide gated cation channel with six
CC transmembrane domains. HBMYCNG genes are useful for treating ion channel-
CC related disorders, e.g. stroke, anxiety and depression, Alzheimer's or
CC Parkinson's disease, arrhythmia, diabetes, chronic pain, hypercalcaemia,
CC hypocalcaemia, hypercalciuria, hypocalciuria, gastrointestinal disorders,
CC ion disorders or renal or liver disease
XX
SQ Sequence 664 AA;
Query Match 97.4%; Score 3384; DB 5; Length 664;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 648; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
QY 1 MTEKSNVGVKSSPANNHHPSPSIKANGKDDHRRAGSRPQSVAAADDTSPQLQRLAEMDT 60
Db |||||
QY 1 MTEKSNVGVKSSPANNHHPSPSIKANGKDDHRRAGSRPQSVAAADDTSPQLQRLAEMDT 60
Db |||||
QY 61 PRRGGGFORIVRLGVIRDWANKNPREPRPDSFLERFRGPELQTVTHQDDKGGKD 120
Db |||||
QY 61 PRRGGGFORIVRLGVIRDWANKNPREPRPDSFLERFRGPELQTVTHQDDKGGKD 120
Db |||||
QY 121 GSGGKTKKXKPELVLDPAAGDWYRMLFVIAMPVLYNWCLLVARACFSDLQRYFVWVLVL 180
Db |||||
QY 121 GSGGKTKKXKPELVLDPAAGDWYRMLFVIAMPVLYNWCLLVARACFSDLQRYFVWVLVL 180
Db |||||
QY 181 DYFSTVYIADLIIRLTGFLQGLLVKDPKLRDNYIHTLQPKLDVASIITDILYFVAV 240
Db |||||
QY 181 DYFSTVYIADLIIRLTGFLQGLLVKDPKLRDNYIHTLQPKLDVASIITDILYFVAV 240
Db |||||
QY 241 GHSPVRENRLHFARMEFFDRTETRTSYNIFRISNLVLYLVIHWNACIYYVSKS 300
Db |||||
QY 241 GHSPVRENRLHFARMEFFDRTETRTSYNIFRISNLVLYLVIHWNACIYYVSKS 300
Db |||||
QY 301 STGFQVDTWVYVNIITDPEYGYLAREYIYCLYXSTLTLTGTTPPVKDEYLFVIFDL 360
Db |||||
QY 301 STGFQVDTWVYVNIITDPEYGYLAREYIYCLYXSTLTLTGTTPPVKDEYLFVIFDL 360
Db |||||
QY 361 IGVLIPTATVGVNGSMISNNATRAEFQAKIDAVKHYMQFRKVSQDMEAKVTKWFDYLT 420
Db |||||
QY 361 IGVLIPTATVGVNGSMISNNATRAEFQAKIDAVKHYMQFRKVSQDMEAKVTKWFDYLT 420
Db |||||
QY 421 NKKTVDEREVLKPLAKLRAEIAINVHLSLTKKVRIFQDWEAGLVVLELVKLRPQVFSFG 480
Db |||||
QY 421 NKKTVDEREVLKPLAKLRAEIAINVHLSLTKKVRIFQDWEAGLVVLELVKLRPQVFSFG 480
Db |||||
QY 481 DYICRKGDITGKEMYYIKEGKLAVVADGVTQVALLSAGSCFGEISILNTKSGMGNRRTA 540
Db |||||
QY 481 DYICRKGDITGKEMYYIKEGKLAVVADGVTQVALLSAGSCFGEISILNTKSGMGNRRTG 540
Db |||||
QY 541 NIRSGLYSDFCLSKDDLMEAVTEAPDAKKVLEERGSEILMKWGLLDENEVAASMEVDVQ 600
Db |||||
QY 541 TIRSLGYSDFCLSKDDLMEAVTEAPDAKKVLEERGSEILMKWGLLDENEVAASMEVDVQ 600
Db |||||
QY 601 EKLEQLETNMDTLTYTFARLLAETGCAQKQLKQITVLETMKQNHEDDYLSDGINTPEP 660
Db |||||
QY 601 EKLEQLETNMDTLTYTFARLLAETGCAQKQLKQITVLETMKQNHEDDYLSDGINTPEP 660
Db |||||
QY 661 TAAE 664
Db ||
QY 661 AVAE 664
Db ||

RESULT 9
AAG79526

ID AAG79526 standard; protein; 732 AA.
XX
AC AAG79526;
XX
DT 09-DEC-2002 (first entry)
XX
DE Rabbit HBMYCNG.
XX
KW Human; cation channel; cyclic nucleotide gated; HBMYCNG;
KW ion channel-related disorder; stroke; depression; liver disease;
KW Alzheimer's disease; Parkinson's disease; arrhythmia; diabetes;
KW chronic pain; hypercalcaemia; hypocalcaemia; hypercalciuria; anxiety;
KW hypocalciuria; gastrointestinal disorder; renal disease.
XX
OS Oryctolagus cuniculus.
XX
FN WO200268471-A2.
XX
PD 06-SEP-2002.
XX
PF 21-DEC-2001; 2001WO-US050413.
XX
PR 21-DEC-2000; 2000US-0257865P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Feder J, Mintier G, Ramanathan C, Westphal R;
XX
DR WPI; 2002-691655/74.
XX
PT New human HBMYCNG genes, useful for treating ion channel-related
PT disorders e.g. stroke, anxiety and depression, Alzheimer's or Parkinson's
PT disease, diabetes or arrhythmia.
XX
PS Disclosure; Fig 4; 177pp; English.
XX
CC The sequences given in AAG79526-29 represent rabbit, cow, mouse and rat
CC versions of the human cation channel polypeptide designated HBMYCNG.
CC HBMYCNG is a human cyclic nucleotide gated cation channel with six
CC transmembrane domains. HBMYCNG genes are useful for treating ion channel-
CC related disorders, e.g. stroke, anxiety and depression, Alzheimer's or
CC Parkinson's disease, arrhythmia, diabetes, chronic pain, hypercalcaemia,
CC hypocalcaemia, hypercalciuria, hypocalciuria, gastrointestinal disorders,
CC ion disorders or renal or liver disease
XX
SQ Sequence 732 AA;
Query Match 93.0%; Score 3231.5; DB 5; Length 732;
Best Local Similarity 93.8%; Pred. No. 3e-309;
Matches 622; Conservative 16; Mismatches 24; Indels 1; Gaps 1;
QY 2 MTEKSNVGVKSSPANNHHPSPSIKANGKDDHRRAGSRPQSVAAADDTSPQLQRLAEMDTP 61
Db |||||
QY 69 MTEKSNVGVKSSPANNHHPSPSIKANGKDDHRRAGSRPQSVAAADDTSPQLQRLAEMDAP 127
Db |||||
QY 62 RRGGRGFORIVRLGVIRDWANKNPREPRPDSFLERFRGPELQTVTHQDDKGGKDG 121
Db ::|||
QY 128 QRRGGRFIVRLGVIRDWANKNPREPRPDSFLERFRGPELQTVTHQDDKGGKDG 187
Db |||||
QY 122 BGKGTNKKXKPELVLDPAAGDWYRMLFVIAMPVLYNWCLLVARACFSDLQRYFVWVLVD 181
Db |||||
QY 188 DGKGTNKKXKPELVLDPAAGDWYRMLFVIAMPVLYNWCLLVARACFSDLQRYFVWVLVD 247
Db |||||
QY 182 YFSDTVYIADLIIRLTGFLQGLLVKDPKLRDNYIHTLQPKLDVASIITDILYFVAV 241
Db |||||
QY 248 YFSDTVYIADLIIRLTGFLQGLLVKDPKLRDNYIHTLQPKLDVASIITDILYFVAV 307
Db |||||
QY 242 IHSPEVRENRLHFARMEFFDRTETRTSYNIFRISNLVLYLVIHWNACIYYVSKS 301
Db |||||
QY 308 IHNPELRNRLHFARMEFFDRTETRTSYNIFRISNLVLYLVIHWNACIYYVSKS 367
Db |||||
QY 302 IGFQVDTWVYVNIITDPEYGYLAREYIYCLYXSTLTLTGTTPPVKDEYLFVIFDL 361
Db |||||

Db 368 IGFGVDTWVYPNITDPEYGYLAREYICLYWSTLTITIGETPPPVKDBEYLFVIFDFLI 427
 QY 362 GVLIFATIVGVNMGSMISNNATRAEFAQAKIDAVKHYMQFRKYSKDEAKVIKWFEDYLWLN 421
 Db 428 GVLIFATIVGVNMGSMISNNATRAEFAQAKIDAVKHYMQFRKYSKDEAKVIKWFEDYLWLN 487
 QY 422 KKTVDEREVLKPKLPAKRAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKLRPQVFSFGD 481
 Db 488 KKTVDEREVLKPKLPAKRAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKLRPQVFSFGD 547
 QY 482 YICRKGDIKEMWIIKEGKLAVVADDGVTQYALLSAGSCFGEISILINIKSGSKGNRRRTAN 541
 Db 548 YICRKGDIKEMWIIKEGKLAVVADDGVTQYALLSAGSCFGEISILINIKSGSKGNRRRTAN 607
 QY 542 IRSLGYSDLFCLSKODLMEAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQE 601
 Db 608 IRSLGYSDLFCLSKODLMEAVTEYPAKKVLEERGREILMKGLLDENEVAASMEVDVQE 667
 QY 602 KLEQLETNMDTLYTRFARLLAEYTGQOKLKORITVLETKMKQNHEDDYLSDGINTPEPT 661
 Db 668 KLEQLETNMDTLYTRFARLLAEYTGQOKLKORITVLETKMKQNHEDDYLSDGMSPEPA 727
 QY 662 AAE 664
 Db 728 AAE 730
 RESULT 10
 AAG79527
 ID AAG79527 standard; protein; 663 AA.
 XX
 AC AAG79527;
 DT 09-DEC-2002 (first entry)
 DE Cow HBMVCNG.
 XX Human; cation channel; cyclic nucleotide gated; HBMVCNG;
 KW ion channel-related disorder; stroke; depression; liver disease;
 KW Alzheimer's disease; Parkinson's disease; arrhythmia; diabetes;
 KW chronic pain; hypercalcaemia; hypocalcaemia; hypercalciuria; anxiety;
 KW hypocalciuria; gastrointestinal disorder; renal disease.
 XX Bos taurus.
 OS
 XX WO200268471-A2.
 PN
 PD 06-SEP-2002.
 PF 21-DEC-2001; 2001WO-US050413.
 PR 21-DEC-2000; 2000US-0257865P.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Feder J, Mintier G, Ramanathan C, Westphal R;
 XX WPI; 2002-691655/74.
 DR
 PT New human HBMVCNG genes, useful for treating ion channel-related
 PT disorders e.g. stroke, anxiety and depression, Alzheimer's or Parkinson's
 PT disease, diabetes or arrhythmia.
 XX
 PS Disclosure; Fig 4; 177pp; English.
 XX The sequences given in AAG79526-29 represent rabbit, cow, mouse and rat
 CC versions of the human cation channel polypeptide designated HBMVCNG.
 CC HBMVCNG is a human cyclic nucleotide gated cation channel with six
 CC transmembrane domains. HBMVCNG genes are useful for treating ion channel-
 CC related disorders, e.g. stroke, anxiety and depression, Alzheimer's or
 CC Parkinson's disease, arrhythmia, diabetes, chronic pain, hypercalcaemia,
 CC hypocalcaemia, hypercalciuria, hypocalciuria, gastrointestinal disorders,
 CC ion disorders or renal or liver disease

XX Sequence 663 AA;
 SQ
 Query Match 92.2%; Score 3204.5; DB 5; Length 663;
 Best Local Similarity 92.3%; Pred. No. 1.2e-306;
 Matches 610; Conservative 27; Mismatches 23; Indels 1; Gaps 1;
 QY 2 MTEKNGVKSPANNHHPSPSIKANGKDDHRAGSRPQSVAAADDTSPELQRLAEMDTP 61
 Db 1 MTEKANGVKSPANNHHPAPAIKASGKDDHRASSRPQSAAD-DTSSQLQQLAEMDAP 59
 QY 62 RRGCGGFORIVLVGVIRDWANKNFRPEEPDPSFLERPRGPELQTVTTTHQDDKGGKDG 121
 Db 60 QORRGGFRIARLVGLREWAYRNERPEEPDPSFLERPRGPELHTVTITQQDGGKGGKDG 119
 QY 122 EGKGTKKKPELVLDPAQDWYRMLFVIAMPVLYNWCILLVARACFSDFQRNVFVWLVLD 181
 Db 120 EGKGTKKKPELVLDPAQDWYRMLFLIALPVLYNWCILLVARACFSDFQKGYIYVWLVLD 179
 QY 182 YFSDTVYIADLIIRLTGTFLEQGLLVKDPKKLRDNYIHTLOFKLDVASIITPDLLYFVAVG 241
 Db 180 YVSDVVIADLIIRLTGTFLEQGLLVKDTKKLRDNYIHTMQPKLDVASIITPDLLYFVAVG 239
 QY 242 IHSPEVRNRLHFAFMPEFFDRTETRTSYNMFRIISNLVLYILVIHWNACIYVVISKS 301
 Db 240 IHNPEVRNRLHFAFMPEFFDRTETRTSYNMFRIISNLVLYILVIHWNACIYVVISKS 299
 QY 302 IGFGVDTWVYPNITDPEYGYLAREYICLYWSTLTITIGETPPPVKDBEYLFVIFDFLI 361
 Db 300 IGFGVDTWVYPNITDPEYGYLSREYIYCLYWSTLTITIGETPPPVKDBEYLFVIFDFLI 359
 QY 362 GVLIFATIVGVNMGSMISNNATRAEFAQAKIDAVKHYMQFRKYSKDEAKVIKWFEDYLWLN 421
 Db 360 GVLIFATIVGVNMGSMISNNATRAEFAQAKIDAVKHYMQFRKYSKDEAKVIKWFEDYLWLN 419
 QY 422 KKTVDEREVLKPKLPAKRAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKLRPQVFSFGD 481
 Db 420 KKSVDEREVLKPKLPAKRAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKLRPQVFSFGD 479
 QY 482 YICRKGDIKEMWIIKEGKLAVVADDGVTQYALLSAGSCFGEISILINIKSGSKGNRRRTAN 541
 Db 480 YICRKGDIKEMWIIKEGKLAVVADDGVTQYALLSAGSCFGEISILINIKSGSKGNRRRTAN 539
 QY 542 IRSLGYSDLFCLSKODLMEAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQE 601
 Db 540 IRSLGYSDLFCLSKODLMEAVTEYPAKKVLEERGREILMKGLLDENEVAASMEVDVQE 599
 QY 602 KLEQLETNMDTLYTRFARLLAEYTGQOKLKORITVLETKMKQNHEDDYLSDGINTPEPT 661
 Db 600 KLEQLETNMDTLYTRFARLLAEYTGQOKLKORITVLETKMKQNHEDDYLSDGMSPEPP 659
 QY 662 A 662
 Db 660 A 660
 RESULT 11
 ABG74912
 ID ABG74912 standard; protein; 663 AA.
 XX
 AC ABG74912;
 XX
 DT 10-JUL-2003 (first entry)
 DE Bovine CNG ion channel alpha3 subunit.
 XX CNG ion channel; alpha3 subunit; phosphodiesterase; drug screening;
 KW cyclic nucleotide gated ion channel; CAMP sensitivity; adenylyl cyclase;
 KW cyclic adenosine monophosphate; cyclic guanosine monophosphate; bovine;
 KW G protein-coupled receptor; calcium concentration.
 XX
 OS Bos taurus.
 XX

Search completed: May 12, 2004, 11:13:44
Job time : 52 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 12, 2004, 11:12:35 ; Search time 23 seconds
(without alignments)
1490.419 Million cell updates/sec

Title: US-10-087-217a-8
Perfect score: 3475
Sequence: 1 MMTEKSGVYKSPANNHH.....NHEDDYLSDGINTPEPTAAE 664

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2.6/prodata/2/iaa/5A COMB.pep: *
2: /cgn2.6/prodata/2/iaa/5B COMB.pep: *
3: /cgn2.6/prodata/2/iaa/6A COMB.pep: *
4: /cgn2.6/prodata/2/iaa/6B COMB.pep: *
5: /cgn2.6/prodata/2/iaa/6CTUS COMB.pep: *
6: /cgn2.6/prodata/2/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2030	58.4	690	4	US-09-275-252A-19
2	1323	38.1	261	4	US-09-275-252A-18
3	634	18.2	129	4	US-08-997-685A-46
4	584	16.8	170	4	US-09-358-383C-27
5	573.5	16.5	126	4	US-08-997-685A-58
6	532.5	15.3	319	4	US-09-358-383C-22
7	526.5	15.2	126	4	US-08-997-685A-57
8	523.5	15.1	910	4	US-08-997-685A-2
9	513	14.8	749	4	US-08-997-685A-10
10	486.5	14.0	528	4	US-08-997-685A-4
11	474	13.6	537	4	US-08-997-685A-12
12	448	12.9	506	4	US-08-997-685A-6
13	446	12.8	988	4	US-09-614-480-2
14	446	12.8	988	4	US-10-162-012-5
15	440	12.7	988	4	US-10-162-012-12
16	424.5	12.2	962	4	US-09-614-480-9
17	424.5	12.2	962	4	US-09-694-777A-3
18	423.5	12.2	962	4	US-09-694-777A-24
19	423	12.2	960	4	US-09-694-777A-21
20	417	12.0	989	4	US-09-694-777A-4
21	416	12.0	989	4	US-09-694-777A-23
22	415.5	12.0	987	4	US-09-694-777A-22
23	413	11.9	1102	4	US-09-358-383C-36
24	407.5	11.7	1284	4	US-09-343-494-9
25	407.5	11.7	1284	4	US-08-358-383C-11
26	401	11.5	1107	4	US-09-358-383C-16
27	394	11.3	1159	2	US-08-956-242-13

28	394	11.3	1159	3	US-09-351-215-13	Sequence 13, Appl
29	394	11.3	1159	3	US-09-226-012-2	Sequence 2, Appl
30	394	11.3	1159	3	US-09-226-012-4	Sequence 4, Appl
31	394	11.3	1159	4	US-09-358-383C-10	Sequence 10, Appl
32	394	11.3	1159	4	US-09-275-252A-12	Sequence 12, Appl
33	390.5	11.2	888	2	US-08-956-242-4	Sequence 4, Appl
34	390.5	11.2	888	3	US-09-351-215-4	Sequence 4, Appl
35	385.5	11.1	1017	4	US-09-600-776-6	Sequence 6, Appl
36	381.5	11.0	1083	4	US-09-600-776-2	Sequence 2, Appl
37	381.5	11.0	1083	4	US-09-343-494-1	Sequence 1, Appl
38	381	11.0	189	4	US-09-358-383C-25	Sequence 25, Appl
39	380	10.9	1083	4	US-09-358-383C-2	Sequence 2, Appl
40	378.5	10.9	1082	4	US-09-336-643A-20	Sequence 20, Appl
41	319.5	9.2	857	4	US-09-275-252A-11	Sequence 11, Appl
42	300	8.6	57	4	US-09-275-252A-38	Sequence 38, Appl
43	286.5	8.2	597	4	US-09-275-252A-7	Sequence 7, Appl
44	265	7.6	57	4	US-09-275-252A-39	Sequence 39, Appl
45	254	7.3	542	4	US-09-358-383C-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-275-252A-19
; Sequence 19, Application US/09275252A
; Patent No. 6641997
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/09/275,252A
; CURRENT FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 19
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-275-252A-19

Query Match	58.4%;	Score 2030;	DB 4;	Length 690;
Best Local Similarity	61.7%;	Pred. No. 9.9e-193;		
Matches 407;	Conservative 84;	Mismatches 131;	Indels 38;	Gaps 7;
QY	23	PSIKANGDDHRRGSRPQSVAAADDTSPLOQLAEMDTFRGRGGF-----QRI 71		
Db	25	PDIE---KEIRWMENGACGSFSDDDSAVTSSESENEP-HARGSFYSKLRKGPSQRE 80		
QY	72	VRLVGVR-----DWANKPREPEPRPDSFLERPRGPELTQVTTHQDDKG 117		
Db	81	QYLPGAIAIFNVNNSNKDQEPPEKKKKKKKKKKKKKKKKKKKKKKKKKKKK 136		
QY	118	GKDGEKGTKK---KFELFLVDPAGDWYRWLFVIAFVLPVYNWCLLVARACFSDIQRNY 173		
Db	137	KKKKEKSKDKKHHKKEVVVDPSGNTYNNWLFCTLPVWNVTWVIARACFDELOQSY 196		
QY	174	FVWVLVDYFSTVVIADLIIRLTGFEQGLVQKDPKKLRDNYTHLQFKLDVASIIFT 233		
Db	197	LEWVILDYVSDIVVYLDIMFVTRTGYLEQGLLVKEELKLNKYSNLQFKLDVLSIPT 256		
QY	234	DLIYFVANGHSBEVFNRLHFAFPEFDRTRTTSYNIFRISNLVILYILVIHWNAC 293		
Db	257	DLLYFKLGNWYFEIRLNRLRFSRMFEFFQRTETRTNYENIFRISNLVYIIVIIHWNAC 316		

QY 294 IYVVISKISGFGVDTWVYPNITDPYGYLAREYICLYWSTLTTLTTIGETPPPVKDBEYL 353
Db 317 VFTSISKAIGFNDTWYIPDINDEFGLARKYVYSYWNSTLTTLTTIGETPPPVKDBEYL 376
QY 354 FVIFDFLIGLIVFATIVGVNIGSMISNNNATRAEFQAKIDAVKHVMQPRKYSKDMKAEKVIK 413
Db 377 FVVVDFLIGLIVFATIVGVNIGSMISNNNATRAEFQAKIDAVKHVMQPRKYSKDMKAEKVIK 436
QY 414 WFDYLTWTKTVDREVLKPKLRAEIAINVLSTLTKKVRIPQDWEAGLLVELVLKLR 473
Db 437 WFDYLTWTKTVDREVLKPKLRAEIAINVLSTLTKKVRIPQDWEAGLLVELVLKLR 496
QY 474 PQVPSPDYICRKGDIKGMWIIKEGKLVAVDDGVTOYALLSAGSCFGEISILINIKGSK 533
Db 497 PQVPSPDYICRKGDIKGMWIIKEGKLVAVDDGVTOYALLSAGSCFGEISILINIKGSK 556
QY 534 MGNRTANIRSLGSDYDFCLSKDLMBAVTEAPDAKKVLEERREILMKMLLDENEV-A 592
Db 557 AGNRRTANIKSIGSDYDFCLSKDLMBAVTEAPDAKKVLEERREILMKMLLDENEV-A 616
QY 593 ASMEVDVQEKLEQLETWMDTLYTFARLLAEYTGAAQOKLQRTVLETKMKQNHEDDYL 652
Db 617 GSDPKDLEKXVTRMEGSDVLLQTRFARILAEYESMOOKLQRLTKVEKFLKPLIDTFESS 676
RESULT 2
US-09-275-252A-18
; Sequence 18, Application US/09275252A
; Patent No. 6641997
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/09/275,252A
; CURRENT FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-275-252A-18

Query Match 38.1%; Score 1323; DB 4; Length 261;
Best Local Similarity 97.7%; Pred. No. 4.3e-123;
Matches 255; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 294 IYVVISKISGFGVDTWVYPNITDPYGYLAREYICLYWSTLTTLTTIGETPPPVKDBEYL 353
Db 1 IYVVISKISGFGVDTWVYPNITDPYGYLAREYICLYWSTLTTLTTIGETPPPVKDBEYL 60
QY 354 FVIFDFLIGLIVFATIVGVNIGSMISNNNATRAEFQAKIDAVKHVMQPRKYSKDMKAEKVIK 413
Db 61 FVIFDFLIGLIVFATIVGVNIGSMISNNNATRAEFQAKIDAVKHVMQPRKYSKDMKAEKVIK 120
QY 414 WFDYLTWTKTVDREVLKPKLRAEIAINVLSTLTKKVRIPQDWEAGLLVELVLKLR 473
Db 121 WFDYLTWTKTVDREVLKPKLRAEIAINVLSTLTKKVRIPQDWEAGLLVELVLKLR 180
QY 474 PQVPSPDYICRKGDIKGMWIIKEGKLVAVDDGVTOYALLSAGSCFGEISILINIKGSK 533
Db 181 PQVPSPDYICRKGDIKGMWIIKEGKLVAVDDGVTOYALLSAGSCFGEISILINIKGSK 240

QY 534 MGNRTANIRSLGSDYDFCLSK 554
Db 241 MGNRTANIRSLGSDYDFCLSK 261
RESULT 3
US-08-997-685A-46
; Sequence 46, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 129
; TYPE: PRT
; ORGANISM: rat;
; FEATURE:
; NAME/KEY: NON CONS
; LOCATION: (48)..(49)
; OTHER INFORMATION: gap in alignment
; FEATURE:
; NAME/KEY: NON CONS
; LOCATION: (121)..(122)
; OTHER INFORMATION: gap in alignment
; FEATURE:
; NAME/KEY: NON CONS
; LOCATION: (125)..(126)
; OTHER INFORMATION: gap in alignment
US-08-997-685A-46
Query Match 18.2%; Score 634; DB 4; Length 129;
Best Local Similarity 98.4%; Pred. No. 4.6e-55;
Matches 127; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 464 LLVELVLKLRPQVSPDYICRKGDIKGMWIIKEGKLVAVDDGVTOYALLSAGSCFGE 523
Db 1 LLVELVLKLRPQVSPDYICRKGDIKGMWIIKEGKLVAVDDGVTOYALLSAGSCFGE 60
QY 524 ISILINIKSGMGNRTANIRSLGSDYDFCLSKDLMBAVTEAPDAKKVLEERREILMKM 583
Db 61 ISILINIKSGMGNRTANIRSLGSDYDFCLSKDLMBAVTEAPDAKKVLEERREILMKM 120
QY 584 GLLDENEVA 592
Db 121 GLLDENEVA 129
RESULT 4
US-09-358-383C-27
; Sequence 27, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/09/358,383C
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: domain


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Query Match      14.0%; Score 486.5; DB 4; Length 528;
Best Local Similarity 26.6%; Pred. No. 2.2e-39;
Matches 133; Conservative 109; Mismatches 203; Indels 55; Gaps 17;

Qy      121 GEGGTGKKKE-----LFVLDPAGDWYRMLFVIAMPVLYNWCLL-VARACFSDLQRY 173
Db      8 GSQKAVREOERVKSGAWIIHPYSDERFYWDFTMLEFVGNGLIIPVGITFFKD---ET 64

Qy      174 FVWMLVDYFSDTYVADIIRLTGFL--EQLLVKDKPKLRDNVYHTLOQKLDVASII 231
Db      65 TAPWIVENVVSDTFELMDVLNFRIGVIENTEILDPKIKKKYLT-WEVVDVFSII 123

Qy      232 PTDUIYFAV--GIHSPVPR-----FNRLHFARMPEFFDRTE-----TRT 269
Db      124 PVDYIFLIVEKIDSEVVKATARALRVPTKILSLRLRLSLRLRYTHQWBEIFHMTVD 183

Qy      270 SYPNIFRISNLVLIILHWNACIYYVISKISGFGVDTWV-YPNITDPEYGLAREYII 328
Db      184 LASAVMRICNLISWMMLLCHWDGCLQFLVPMQLDPPSCWYSINNMVHNSWSEL---YSF 240

Qy      329 CLYVSTLTLTATIG---ETPPVPKDEEYLFVIFDFLIGLIVFIATVGNVGSIMSNMNA 385
Db      241 ALFKAMSHMLCIGYGRQAPESMTD--IWLTMLSMIVGATCAMFGHATALLQSLDSRR 298

Qy      386 EFOAKIDAVKHMYOFKRVSKDMEAKVIKWFDYLTNNKTVDEREVLKNLPKLAKEIAIN 445
Db      299 QYQEKYQVEQYMSFHKLPAQFRQKIDHYEHRYQKMS--DEDSILGELNGPLREEI-VN 356

Qy      446 VHLSTL-KKVRIFODWAGLLVELVLKLRPOVFSFGDYICRKGDIGKEMYIIKEGLAV 504
Db      357 FNCRKLVASPLFANADPNFVTAMLTCLKFEVFOFGDYIIREGTIGKMYFTIQHGVSV 416

Qy      505 ADDGVTOYALLSAGSCFGEISILNIKSGKGNRRNTANIRSLGYSDLFCLSKDDLMEAVTE 564
Db      417 TKG--NKEMKLSDSYSGEICLLT-----RGRRTASVRATYCRKLSLSDVDFNEVLEE 468

Qy      565 APDAKKVLEERGERILMKMG 584
Db      469 YPMRRRAFETVAIDRLDRIG 488

RESULT 11
US-08-997-685A-12
; Sequence 12, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 597
; TYPE: PRT
; ORGANISM: human;
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AAC39760
; DATABASE ENTRY DATE: 1998-05-29
; RELEVANT RESIDUES: (1)..(597)
US-08-997-685A-12

Query Match      13.6%; Score 474; DB 4; Length 597;
Best Local Similarity 26.9%; Pred. No. 4.7e-38;
Matches 144; Conservative 111; Mismatches 216; Indels 64; Gaps 21;

Qy      90 EPRPD--SELRFRGPELOQTVTHQGDCKG--KDGEKGTKKKFE-----LFVLDPAG 139
Db      8 EPGSQASFWORQFGALLQ-----PGVNNKSLRMFGSQKAVREOERVKSGAWIIHPYS 62

Qy      140 DWYRMLFVIAMPVLYNWCLL-VARACFSDLQRYFVWMLVDYFSDTYVADIIRLT 198

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Db 63 DFRFYDFTMLLRWVGNLIIPVGIETFKD---ETAPWIVFNWVSDTFELMDLVNFT 119
QY 199 GEL--EGLAVKPKLRDNYIHTLOFKLDVASIIPDILYFV--GIHSPE----- 246
Db 120 GIVIEDTEIILDEPKIKKKYLR--WFVVVFSIPVDYIFLIVKEGIDSEVYKARAL 178
QY 247 -VRFN-----RLHFARMEFFDRTE-----TRTSYPNIFRISNLVLYIIVIHWNACI 294
Db 179 IVRFTKLSLRLRLSLRYIHQWEEIFHMTYDLASAVNRICNLISMLLCHWDGCL 238
QY 295 YVVISKISIGFVDTWVYPN--ITDPEYGLAREYIYCLYWSLTTLTTIG--ETPPPVKDE 350
Db 239 QELVPMLODFPRNCWWSINGMVNWSSEL---XSFALFKAMSHMLCIGYGRQAPVMS 294
QY 351 EYLFVIFDFLIGLIVFATIVGNVSMISNNATRAEFOAKIDAVKHYMQFRKYSKMEAK 410
Db 295 -IWLTMISMIVGATCYAMFIGHATALIQSLDSRRQYQEKYQVQYMSFHKLPADFRQK 353
QY 411 VIKWFDYLTNKKTVDBREVILKXLPKALRAEIAINVHLSL--KKVRIQDWEAGLLVELV 469
Db 354 IHDIYEHRYQG--KMFDEDSILGELNGPLREEI--VNFNCRKLVASMPPLFANADPNFVTAML 411
QY 470 LKLRPQVSPGDYICRKGDIKEMYYIKKGLAVVADDGVTQYALLSAGSCFGEISILNI 529
Db 412 TKLRFVFPQGDYIIRSTIGTKMYFIQHGVSVLTKG--NKEMKJSDGSYFGEICLLT- 468
QY 530 KSKMGNRRNTANIRSLGSDLCFLSKDDLMLEAVEAPDAKKVLEERGEREILMKMG 584
Db 469 -----RGRRTASVRADTYCRLYSLVSDNFNEVLEEYPMRRAFETVAIDRLDRIG 518

RESULT 12
US-08-997-685A-6
; Sequence 6, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 506
; TYPE: PRT
; ORGANISM: mouse;
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AAC40126
; DATABASE ENTRY DATE: 1998-05-29
; RELEVANT RESIDUES: (1)..(506)
US-08-997-685A-6

Query Match 12.9%; Score 448; DB 4; Length 506;
Best Local Similarity 25.0%; Pred. No. 1.4e-35;
Matches 141; Conservative 111; Mismatches 212; Indels 100; Gaps 22;

QY 24 SIKANGKDDHRAGSRPQSVAADDTSPELQRLAEMDTPRGRGGFQRIVLVGVIRWAN 83
Db 9 AIKVEG-----GAAAIHILPE---REV---RLQSGFMQ--RQFGAML----- 44
QY 84 KNFREESRPDSFLERFRGPELQVTTTHQGDGKGDEGKGTKKPE-----LFVLDP 137
Db 45 -----QGVNKFSLRMFGSQ-----KAVEREQERVKSAGFWIHP 79
QY 138 AGDWYELFVIAVMPVLYNCLL--VARACFSDIQRNVFVWLVLDYSDTVYIADLIIRL 196
Db 80 YSDFRFTYDNLTMLLMVGNIILIPVGIITFKD---ENTTFWIVFNWVSDTFELDLVINF 136
QY 197 RTGFL--EQGLLVKDKPKLRDNYIHTLOFKLDVASIIPDILYFVAVGIHSPE----- 246
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Db 137 RTGIWVEDNTEIILDQRIMKKYKLS--WFVVDFISSIPVEYIFELIVETRIDSEVYKTARA 195
QY 247 ---VRN-----RLHFARMEFFDRTE-----TRTSYPNIFRISNLVLYIIVIHWNACI 294
Db 196 VLRVETKLSLRLRLSLRYIHQWEEIFHMTYDLASAVNRICNLISMLLCHWDG 255
QY 293 CIYVVISKISIGFVDTWVYPN--ITDPEYGLAREYIYCLYWSLTTLTTIG--ETPPPVKDE 350
Db 256 CLQFLVPMLODFPHDCWWSINGMVNWSG---KQSYALFKAMSHMLCIGYGRQAPVMS 312
QY 351 EYLFVIFDFLIGLIVFATIVGNVSMISNNATRAEFOAKIDAVKHYMQFRKYSKMEAK 410
Db 313 DVMLTMLSMIVGATCYAMFIGHATALIQSLDSRRQYQEKYQVQYMSFHKLPADFRQK 372
QY 411 VIKWFDYLTNKKTVDBREVILKXLPKALRAEIAINVHLSL--KKVRIQDWEAGLLVELV 469
Db 373 IHDIYEHRYQG--KMFDEESILGELSEPLREEI--INFNCRKLVASMPPLFANADPNFVTAML 430
QY 470 LKLRPQVSPGDYICRKGDIKEMYYIKKGLAVVADDGVTQYALLSAGSCFGEISILNI 529
Db 431 TKLRFVFPQGDYIIRSTIGTKMYFIQHGVSVLTKG--NKETRLADGSYFGEICLLT- 487
QY 530 KSKMGNRRNTANIRSLGSDLCFL 553
Db 488 -----RGRRTASVRADTYCRLYSL 506

RESULT 13
US-09-614-480-2
; Sequence 2, Application US/09614480
; Patent No. 6586179
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: Liu, Yi
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: Human Bag2
; FILE REFERENCE: 018512-002310US
; CURRENT APPLICATION NUMBER: US/09/614,480
; CURRENT FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: US 60/143,467
; PRIOR FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 988
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-614-480-2

Query Match 12.8%; Score 446; DB 4; Length 988;
Best Local Similarity 25.2%; Pred. No. 6.5e-35;
Matches 150; Conservative 102; Mismatches 220; Indels 124; Gaps 21;

QY 145 WLFVIAVMPVLYNCLLVARACFSDIQRNVFVWLVLDYSDTVYIADLIIRLTGEL-BQ 203
Db 217 WDWIILITFTYTAIVMPVYNVSKTKQNN--IAWLVDSDVVDVIFLVDIVLNFHTTFVPG 274
QY 204 GLIVKDKPKLRDNYIHTLOFKLDVASIIPDILY-----YFVAGIHS--PEVRFNRLLHFAR 257
Db 275 GEVISDPKLIRMYLKT--WFVIDLSCLPYDIINAFENVDEGLISLFSLLKVVRLRLGR 333
QY 258 MFEFFORTETRTSYNIFRISNLVLYV-----IHNACIYVYVSKSIG----- 303
Db 334 VARKLD-----HLEYGAALVLLVCVFLVAHWTACIY-----SIGDYVIDEVT 380
QY 304 --FGVDVTYVYP--NITDPEYGLARE-----YIYCLYWSLTTLTTIG-ETFP 345
Db 381 NTIQDSWLYQALSLGTGP--XYRNTSAGIWEGGPSKDSLYSVSLVFTMTSLTTIGFNIA 439
QY 346 PVKDEYLFVIFDFLIGLIVFATIVGNVSMISNNATRAEFOAKIDAVKHYMQFRKYSK 405
Db 440 PITDVEKMSVAMMVGSLLYATIFGNVTITFQOMYANTNRHMLNVRDFLKYQVPK 499
```


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OM protein - protein search, using sw model

Run on: May 12, 2004, 11:07:49 ; Search time 17 Seconds
(without alignments)
2033.799 Million cell updates/sec

Title: US-10-087-217A-8

Perfect score: 3475

Sequence: 1 MMTEKNGVKSPANNHH.....NHEDYLDGINTPEPTAAE 664

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3449	99.3	664	1	CNG2 RAT
2	3384	97.4	664	1	CNG2 MOUSE
3	3321.5	93.0	664	1	CNG2 RABIT
4	3204.5	92.2	663	1	CNG2 BOVIN
5	2219.5	63.9	735	1	CNG1 CHICK
6	2151.5	61.9	631	1	CNG3 MOUSE
7	2140	61.6	706	1	CNG3 BOVIN
8	2139	61.6	694	1	CNG3 HUMAN
9	2131	61.3	682	1	CNG1 CTPTU
10	2067	59.5	645	1	CNG3 CHICK
11	2044	58.8	690	1	CNG1 BOVIN
12	2034	58.5	686	1	CNG1 HUMAN
13	2026	58.3	683	1	CNG1 RAT
14	2017.5	58.1	691	1	CNG1 CANFA
15	2012.5	57.9	684	1	CNG1 MOUSE
16	1518	43.7	575	1	CNGX RAT
17	1494	43.0	665	1	CNG DROME
18	1338.5	38.5	733	1	CNG CAEEL
19	1323	38.1	261	1	CNG2 HUMAN
20	778	22.4	909	1	CNG4 HUMAN
21	770	22.2	1394	1	CNG4 BOVIN
22	524	15.1	910	1	HCN1 RAT
23	522.5	15.0	910	1	HCN1 MOUSE
24	522	15.0	834	1	HCN2 RAT
25	522	15.0	863	1	HCN2 MOUSE
26	520.5	15.0	822	1	HCN1 RABIT
27	518	14.9	890	1	HCN1 HUMAN
28	484.5	14.2	1203	1	HCN4 HUMAN
29	492	14.2	1198	1	HCN4 RAT
30	490.5	14.1	1175	1	HCN4 RABIT
31	490	14.1	889	1	HCN2 HUMAN
32	481.5	13.9	780	1	HCN3 RAT
33	479	13.8	774	1	HCN3 HUMAN
34	479	13.8	779	1	HCN3 MOUSE
35	475	13.7	1186	1	HCN4 MOUSE
36	446	12.8	988	1	HCN5 HUMAN
37	439	12.6	988	1	HCN5 RAT
38	424.5	12.2	962	1	KCH1 RAT
39	418.5	12.0	950	1	KCH6 RAT
40	418	12.0	1195	1	KCH7 RAT
41	417.5	12.0	1195	1	KCH7 MOUSE
42	417	12.0	989	1	KCH1 HUMAN
43	417	12.0	989	1	KCH1 MOUSE
44	415.5	12.0	987	1	KCH1 BOVIN
45	414.5	11.9	994	1	KCH6 HUMAN

ALIGNMENTS

RESULT 1
CNG2 RAT
ID CNG2 RAT STANDARD; PRT; 664 AA.
AC Q00195;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated
DE cation channel 2) (CNG channel 2) (CNG2) (CNG-2) (OCNCL1).
GN CNGA2 OR CNCG2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory sensory neuron;
RX MEDLINE=90370115; PubMed=1697649;
RA Dhallan R.S., Yau K.-W., Schrader K.A., Reed R.R.;
RT "Primary structure and functional expression of a cyclic nucleotide-
RT activated channel from olfactory neurons.";
RL Nature 347:184-187(1990).
CC -!- FUNCTION: Odorant signal transduction is probably mediated by a G-
CC protein coupled cascade using cAMP as second messenger. The
CC olfactory channel can be shown to be activated by cyclic
CC nucleotides which leads to a depolarization of olfactory sensory
CC neurons.
CC -!- SUBUNIT: Heterooligomer of OCNCL1 and OCNC2 subunits.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Olfactory neurons.
CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
CC (TC 1.A.1.5) family.
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-2 is the initiator.
CC
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CC
CC EMBL; X55519; CAA39135.1; -.
CC PIR; S11517; S11517.
CC InterPro; IPR000595; cNMP binding.
CC InterPro; IPR005821; Ion Trans.
CC InterPro; IPR001622; K+channel pore.
CC Pfam; PF00027; cNMP_binding; 1.
CC Pfam; PF00520; Ion_trans; 1.
CC SMART; SMC0100; cNMP; 1.
CC PROSITE; PS00888; CNMP_BINDING_1; 1.
CC PROSITE; PS00889; CNMP_BINDING_2; 1.
CC PROSITE; PS00442; CNMP_BINDING_3; 1.
CC Ionic channel; Ion transport; cAMP-binding; Transmembrane;
CC Multigene family; Olfaction.
KW

O88705 mus musculu
O70507 mus musculu
O8ncm2 homo sapien
Q9ep19 rattus norv
Q63472 rattus norv
O54853 rattus norv
Q9er47 mus musculu
Q95259 homo sapien
Q60603 mus musculu
O18965 bos taurus
Q9h252 homo sapien

```

FT DOMAIN 1 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 162 H1 (POTENTIAL).
FT DOMAIN 163 175 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 176 194 H2 (POTENTIAL).
FT DOMAIN 195 218 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 219 238 H3 (POTENTIAL).
FT DOMAIN 239 276 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 277 299 H4 (POTENTIAL).
FT DOMAIN 300 351 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 352 371 H5 (POTENTIAL).
FT DOMAIN 372 455 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 456 476 H6 (POTENTIAL).
FT DOMAIN 477 664 CYTOPLASMIC (POTENTIAL).
FT NP BIND 464 586 CAMP (BY SIMILARITY).
FT BINDING 523 538 CAMP (POTENTIAL).
FT BINDING 538 581 CAMP (POTENTIAL).
FT CARBOHYD 381 381 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 212 212 K -> R.
SQ SEQUENCE 664 AA; 76176 MW; 720806950EC27F3C CRC64;

Query Match
Best Local Similarity 99.3%; Score 3449; DB 1; Length 664;
Matches 661; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MMTKSGVGVSSPANNHHPPPSIKANGKDDHAGSRPOSVAADDTSPBLQRLAEMDT 60
Db 1 MMTKSGVGVSSPANNHHPPPSIKANGKDDHAGSRPOSVAADDTSPBLQRLAEMDT 60

Qy 61 PRRGGGFORIVLVGVIRWANKNFRERPDSELERGPELOQTVTTHQGDGKGD 120
Db 61 PRRGGGFORIVLVGVIRWANKNFRERPDSELERGPELOQTVTTHQGDGKGD 120

Qy 121 GEGKGTKKKPELVLDPAAGDWYRWLFVIAFVLYNNCLLVARCFSDLQRYFVWVLV 180
Db 121 GEGKGTKKKPELVLDPAAGDWYRWLFVIAFVLYNNCLLVARCFSDLQRYFVWVLV 180

Qy 181 DYFSDTVIADLIIRLTGTFLBOGLLVKDPKKURDNIHTLOFKLDVASIPTDLIYFV 240
Db 181 DYFSDTVIADLIIRLTGTFLBOGLLVKDPKKURDNIHTLOFKLDVASIPTDLIYFV 240

Qy 241 GIHSPEVRNRLHFARMEFFDRTETRTSPNIFRISNLVLYTLVLIHNACIYYVSK 300
Db 241 GIHSPEVRNRLHFARMEFFDRTETRTSPNIFRISNLVLYTLVLIHNACIYYVSK 300

Qy 301 SIGGVDTWVYVNTDPEYGLAREYIYCLYWSLTLLTTIGETPPPVKDEEYLFVDFL 360
Db 301 SIGGVDTWVYVNTDPEYGLAREYIYCLYWSLTLLTTIGETPPPVKDEEYLFVDFL 360

Qy 361 IGVLIPTIYGVNCSMI SNMNATBAEQAKIDAVKHYMQFRKVSQKDEAKVWFYDYLWT 420
Db 361 IGVLIPTIYGVNCSMI SNMNATBAEQAKIDAVKHYMQFRKVSQKDEAKVWFYDYLWT 420

Qy 421 NKKTVDREVLYKNLPKALRAEIAINVLSTLTKKVRIFQDWEAGLLVELVLRQVPSFG 480
Db 421 NKKTVDREVLYKNLPKALRAEIAINVLSTLTKKVRIFQDWEAGLLVELVLRQVPSFG 480

Qy 481 DYICRKGIDIGEMVIIKEGKLAVVADGVTOYALLSAGSCFGEISILNIGSKMGNRRTA 540
Db 481 DYICRKGIDIGEMVIIKEGKLAVVADGVTOYALLSAGSCFGEISILNIGSKMGNRRTA 540

Qy 541 NIRSIGVSDFLCLSKDDIMEAVTEAPDAKKVLEERGREILMKGLDENEVAASMEVDVQ 600
Db 541 NIRSIGVSDFLCLSKDDIMEAVTEAPDAKKVLEERGREILMKGLDENEVAASMEVDVQ 600

Qy 601 EKLQLENTMDTLTRFARLLAETGAQOKLQRTITVLETKMKONHEDDYLSDGINTPEP 660
Db 601 EKLQLENTMDTLTRFARLLAETGAQOKLQRTITVLETKMKONHEDDYLSDGINTPEP 660

Qy 661 TAEE 664
Db 661 TAEE 664

```

RESULT 2

CNG2_MOUSE STANDARD; PRT; 664 AA.

AC Q62396; DT 01-NOV-1997 (Rel. 35, Last sequence update); DT 01-NOV-1997 (Rel. 35, Last sequence update); DT 15-MAR-2004 (Rel. 43, Last annotation update); DE Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated cation channel 2) (CNG channel 2) (CNG-2) (CNG2); GN CNGA2 OR CNCG2 OR CNCG4; OS Mus musculus (Mouse); OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; OX NCBI_TaxID=10090; RN [1]; RP TISSUE=Heart; RC SEQUENCE FROM N.A.

RX MEDLINE=96439619; PubMed=8841933; RA Ruiz M.L., London B., Nadal-Ginard B.; RT "Cloning and characterization of an olfactory cyclic nucleotide-gated channel expressed in mouse heart."; RL J. Mol. Cell. Cardiol. 28:1453-1461(1996); CC -!- FUNCTION: Odorant signal transduction is probably mediated by a G-protein coupled cascade using cAMP as second messenger. The olfactory channel can be shown to be activated by cyclic nucleotides which leads to a depolarization of olfactory sensory neurons.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel (TC 1.A.1.5) family.

CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.

CC -!- CAUTION: It is uncertain whether Met-1 or Met-2 is the initiator.

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DR EMBL; U49391; AAC52712.1; -. DR GGD; MG1:108040; Cnga2. DR GO; GO:0005216; F:ion channel activity; IMP. DR GO; GO:0007608; P:olfaction; IMP. DR InterPro; IPR000595; cNMP binding. DR InterPro; IPR005821; Ion Trans. DR InterPro; IPR01622; K+channel pore. DR Pfam; PF00027; cNMP binding; 1. DR Pfam; PF00520; Ion trans; 1. DR SMART; SM00100; cNMP; 1. DR PROSITE; PS00888; cNMP BINDING_1; 1. DR PROSITE; PS00889; cNMP BINDING_2; FALSE_NEG. DR PROSITE; PS00890; cNMP BINDING_3; 1. DR KX Ionic channel; Ion transport; CAMP-binding; Transmembrane; KM Multigene family; Olfaction.

FT DOMAIN 1 142 CYTOPLASMIC (POTENTIAL). FT TRANSMEM 143 163 H1 (POTENTIAL). FT DOMAIN 164 175 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 176 194 H2 (POTENTIAL). FT DOMAIN 195 218 CYTOPLASMIC (POTENTIAL). FT TRANSMEM 219 238 H3 (POTENTIAL). FT DOMAIN 239 276 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 277 299 H4 (POTENTIAL). FT DOMAIN 300 351 CYTOPLASMIC (POTENTIAL). FT TRANSMEM 352 371 H5 (POTENTIAL). FT DOMAIN 372 455 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 456 476 H6 (POTENTIAL). FT DOMAIN 477 664 CYTOPLASMIC (POTENTIAL). FT NP BIND 464 586 CAMP (BY SIMILARITY). FT BINDING 523 538 CAMP (POTENTIAL). FT BINDING 538 581 CAMP (POTENTIAL). FT CARBOHYD 381 381 N-LINKED (GLCNAC. . .) (POTENTIAL).

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SQ SEQUENCE 664 AA; 76209 MW; 90B2601D727C6AFE CRC64;
Query Match 97.4%; Score 3384; DB 1; Length 664;
Best Local Similarity 97.6%; Pred. No. 1.9e-218;
Matches 648; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 1 MMTKSNVKSPPANNHHPPSPISKANGKDDHRAGSRPQSVAAADDDTSPQLRLAEMDT 60
Dd 1 MMTKSNVKSPPANNHHPPSPISKANGKDDHRAGSRPQSVAAADDDTSSQLRLAEMDT 60
QY 61 PRRGGGFQRIIVRLGVIRDWANKNFRFEEPRDPSFLERFRGPELQTVTHQGGKGD 120
Dd 61 PRRGGGFRIIVRLGVIRDWANKNFRFEEPRDPSFLERFRGPELQTVTHQGGKGD 120
QY 121 GEGGKTKKFFELFVLDPAGDWYRWLFVIAFVLYNWCLLVARACFSLQRYFVWLVL 180
Dd 121 GEGGKTKKFFELFVLDPAGDWYRWLFVIAFVLYNWCLLVARACFSLQRYFVWLVL 180
QY 181 DYFSDTVVIADLIIRLTGFEQGLLVKDPKILRDNYHTLOFKLDVASIITPTDLYFAV 240
Dd 181 DYFSDTVVIADLIIRLTGFEQGLLVKDPKILRDNYHTLOFKLDVASIITPTDLYFAV 240
QY 241 GIHSPEVRNKLHFAFMFEFFDRTETSTPNFRISNLVLYILVLIHWNACIYVYISK 300
Dd 241 GIHSPEVRNKLHFAFMFEFFDRTETSTPNFRISNLVLYILVLIHWNACIYVYISK 300
QY 301 SIGFGVDTWYPNITDPEYGVLAIEYVCLYWSLTTLTIGETPPPVKDEYLFVDFL 360
Dd 301 SIGFGVDTWYPNITDPEYGVLAIEYVCLYWSLTTLTIGETPPPVKDEYLFVDFL 360
QY 361 IGVLIPTATVGVNCSMISNNNATAEQAIDAVKHYMQFRKVKSKDMEAKVIKWFYDWT 420
Dd 361 IGVLIPTATVGVNCSMISNNNATAEQAIDAVKHYMQFRKVKSKDMEAKVIKWFYDWT 420
QY 421 NKKTVDEREVLKPLAKRAEIALNVHLSLTKVRIQDMEAGLLVELVLRKLPQVPSG 480
Dd 421 NKKTVDEREVLKPLAKRAEIALNVHLSLTKVRIQDMEAGLLVELVLRKLPQVPSG 480
QY 481 DYTCKRGDICKEMVIEKGLAVVADGVTOYALLSAGSCFGEISILNIKSKMGNRTA 540
Dd 481 DYTCKRGDICKEMVIEKGLAVVADGVTOYALLSAGSCFGEISILNIKSKMGNRTG 540
QY 541 NIRSGLYSDFCLSKDLMFAVTEADPAKVLBERGHEILMKGLDENEVAASMEVDVQ 600
Dd 541 TIRSLGYSDFCLSKDLMFAVTEADPAKVLBERGHEILMKGLDENEVAASMEVDVQ 600
QY 601 EKLQLETNMTHTYTRFARLLAETGAQQLKQRIITVLETKMKONHEDDVLSDGINTPEP 660
Dd 601 EKLQLETNMTHTYTRFARLLAETGAQQLKQRIITVLETKMKONHEDDVLSDGINTPEP 660
QY 661 TAAE 664
Dd 661 AVAE 664

RESULT 3
CN2 RABIT STANDARD; PRT; 664 AA.
AC Q287L8;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated
DE cation channel 2) (CN2) (CN2) (Aorta CN2 channel)
DE (RACNG).
GN CN2 OR CN2G2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;

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RX MEDLINE=93359035; PubMed=7689061;
RA Biel M., Altenhofen W., Hulin R., Ludwig J., Freichel M.,
RA Flockerzi V., Dascal N., Kaupp U.B., Hofmann F.;
RT "Primary structure and functional expression of a cyclic nucleotide-
RL gated channel from rabbit aorta.";
RL FEBS Lett. 329:134-138 (1993).
CC 1- FUNCTION: Odorant signal transduction is probably mediated by a G-
CC protein coupled cascade using cAMP as second messenger. The
CC olfactory channel can be shown to be activated by cyclic
CC nucleotides which leads to a depolarization of olfactory sensory
CC neurons.
CC 1- SUBCELLULAR LOCATION: Integral membrane protein.
CC 1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
CC (TC 1.A.1.5) family.
CC 1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC
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CC
CC EMBL; X59668; CAA42201.1; ALT INIT.
DR InterPro; IPR000595; CNMP_binding.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR Pfam; PF00027; CNMP_binding; 1.
DR SMART; SM00100; CNMP; 1.
DR PROSITE; PS00888; CNMP_BINDING_1; 1.
DR PROSITE; PS00889; CNMP_BINDING_2; 1.
DR PROSITE; PS00042; CNMP_BINDING_3; 1.
KW Ionic channel; Ion transport; CAMP-binding; Transmembrane;
KM Multigene family; Olfaction.
FT DOMAIN 1 140 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 141 160 H1 (POTENTIAL).
FT DOMAIN 161 173 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 174 192 H2 (POTENTIAL).
FT DOMAIN 193 216 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 217 236 H3 (POTENTIAL).
FT DOMAIN 237 274 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 275 297 H4 (POTENTIAL).
FT DOMAIN 298 349 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 350 369 H5 (POTENTIAL).
FT DOMAIN 370 453 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 454 474 H6 (POTENTIAL).
FT DOMAIN 475 664 CYTOPLASMIC (POTENTIAL).
FT NP_BIND 462 584 CAMP (BY SIMILARITY).
FT BINDING 521 521 CAMP (POTENTIAL).
FT BINDING 536 536 CAMP (POTENTIAL).
FT CARBOHYD 379 379 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 664 AA; 76205 MW; 5E9170D0B322B3E9 CRC64;

Query Match 93.0%; Score 3231.5; DB 1; Length 664;
Best Local Similarity 93.8%; Pred. No. 2.9e-208;
Matches 622; Conservative 16; Mismatches 24; Indels 1; Gaps 1;

QY 2 MTEKSNVKSPPANNHHPPSPISKANGKDDHRAGSRPQSVAAADDDTSPQLRLAEMDT 61
Dd 1 MTEKSNVKSPPANNHHPPSPISKANGKDDHRAGSRPQSVAAADDDTSPQLRLAEMDT 59
QY 62 PRRGGGFQRIIVRLGVIRDWANKNFRFEEPRDPSFLERFRGPELQTVTHQGGKGD 121
Dd 60 QRRGGFRIIVRLGVIRQWANNFRFEEPRDPSFLERFRGPELQTVTHQGGKGD 119
QY 122 EGKGTKKFFELFVLDPAGDWYRWLFVIAFVLYNWCLLVARACFSLQRYFVWLVL 181
Dd 120 DGKGTKFFELFVLDPAGDWYRWLFVIAFVLYNWCLLVARACFSLQRYFVWLVL 179
QY 182 YFSDTVVIADLIIRLTGFEQGLLVKDPKILRDNYHTLOFKLDVASIITPTDLYFAV 241

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Db 180 YFSVVYIADLIRLRTGFEQGLLVKDPKLRDNYIHTLQFKLDVASIIPDTLIVFVG 239
Qy 242 IHSPEVRNLLHFAFMFEFFRTERTSYPNIRISNLVAVLYLVIHWNACIYVVISKS 301
Db 240 IHNPELRNLLHFAFMFEFFRTERTSYPNIRISNLVAVLYLVIHWNACIYVVISKS 299
Qy 302 IGFGVDTWVYVNTDPEYCYLAREYIYCLYWSLTLTTTIGETPPPVKDEYLVFVDFLI 361
Db 300 IGFGVDTWVYVNTDPEYCYLAREYIYCLYWSLTLTTTIGETPPPVKDEYLVFVDFLI 359
Qy 362 GVLIFATIVGNVSMISNNATRAEFOAKIDAVKHYMPQKYSKMEAKVIRKWFYDLWN 421
Db 360 GVLIFATIVGNVSMISNNATRAEFOAKIDAVKHYMPQKYSKMEAKVIRKWFYDLWN 419
Qy 422 KKTVDREVLKLPKLAKEIAINVHLSLTKKVRIFQDWEAGLLVVLKLRPOVPSGD 481
Db 420 KKTVDREVLKLPKLAKEIAINVHLSLTKKVRIFQDWEAGLLVVLKLRPOVPSGD 479
Qy 482 YICRGDGTGKEMIIKGLAVVADGVTVQYALLSAGSCFGISILNKGSKGNRTAN 541
Db 480 YICRGDGTGKEMIIKGLAVVADGVTVQYALLSAGSCFGISILNKGSKGNRTAN 539
Qy 542 IRSLSYSDLCFLSKDLMKAVTEADAKVLEBERGRELIMKGLDENEVAASMEVDVQE 601
Db 540 IRSLSYSDLCFLSKDLMKAVTEADAKVLEBERGRELIMKGLDENEVAASMEVDVQE 599
Qy 602 KLEQETNMDTLYTRFARLLAETYGAAQKIKORITVLETKMKONHEDDYLSDGINTPST 661
Db 600 KLEQETNMDTLYTRFARLLAETYGAAQKIKORITVLETKMKONHEDDYLSDGMSPEPA 659
Qy 662 AAE 664
Db 660 AAE 662

RESULT 4
ID_CNG2_BOVIN STANDARD; PRT; 663 AA.
AC Q03041;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated
DE cation channel 2) (CNG channel 2) (CNG-2) (CNG2).
GN CNGA2 OR CNCG2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
EN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory epithelium;
RX MEDLINE=91032022; PubMed=1699793;
RA Ludwig J., Margalit T., Eismann E., Lancet D., Kaupp U.B.;
RT "Primary structure of CAMP-gated channel from bovine olfactory
RT epithelium.";
RL FEBS Lett. 270:24-29 (1990).
CC -!- FUNCTION: Odorant signal transduction is probably mediated
CC by a G-protein coupled cascade using cAMP as second messenger.
CC The olfactory channel can be shown to be activated by cyclic
CC nucleotides which leads to a depolarization of olfactory
CC sensory neurons.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Olfactory neurons.
CC -!- MISCELLANEOUS: The olfactory channel is activated by both cAMP and
CC cGMP at similar concentrations, whereas the cGMP-gated channel is
CC much less sensitive to cAMP.
CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
CC (TC 1.A.1.5) family.
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X55010; CAA38754.1; -.
CC PIR; S11521; S11521.
CC InterPro; IPR00595; cNMP_binding.
CC InterPro; IPR005821; Ion_Trans.
CC InterPro; IPR001622; K_channel_pore.
CC Pfam; PF00027; cNMP_binding; 1.
CC Pfam; PF00520; Ion_Trans; 1.
CC SMART; SM00100; cNMP; 1.
CC PROSITE; PS00888; cNMP_BINDING_1; 1.
CC PROSITE; PS00889; cNMP_BINDING_2; 1.
CC PROSITE; PS0042; cNMP_BINDING_3; 1.
CC KW Ionic channel; Ion transport; cAMP-binding; Transmembrane;
CC Multigene family; Olfaction; Glycoprotein.
CC DOMAIN 1 140
CC TRANSMEM 141 160 H1 (POTENTIAL).
CC DOMAIN 161 173 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 174 192 H2 (POTENTIAL).
CC DOMAIN 193 216 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 217 236 H3 (POTENTIAL).
CC DOMAIN 237 274 H4 (POTENTIAL).
CC TRANSMEM 275 297 EXTRACELLULAR (POTENTIAL).
CC DOMAIN 298 349 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 350 369 H5 (POTENTIAL).
CC DOMAIN 370 453 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 454 474 H6 (POTENTIAL).
CC DOMAIN 475 663 CYTOPLASMIC (POTENTIAL).
CC NP_BIND 462 584 CAMP (BY SIMILARITY).
CC BINDING 521 521 CAMP (BY SIMILARITY).
CC BINDING 536 536 CAMP (BY SIMILARITY).
CC CARBOHYD 379 379 N-LINKED (GLCNAC...) (PROBABLE).
CC SEQUENCE 663 AA; 76014 MW; AB66D4F9203844EF CRC64;

Query Match 92.2%; Score 3204.5; DB 1; Length 663;
Best Local Similarity 92.3%; Pred. No. 1.8e-206;
Matches 610; Conservative 27; Mismatches 23; Indels 1; Gaps 1;

Qy 2 MTEKNGVKSPANNHHPSPSIKANGKDDHAGSPQSVAAADDTSPELQIAEMDTP 61
Db 1 MTEKANGVKSPANNHHPAIPAKASGKDDHRASSRPQSAAD-DTSSSELQIAEMDAP 59
Qy 62 RRGGRGGFQRIIVRLGVIRDWANKNFRPEPRPDSFLERERGPPELOQVTHQGDGKGGK 121
Db 60 QQRGGGFRTARLVGLVREWAYNFRPEPRPDSFLERFRGPPELHVTVOQDGGKGGK 119
Qy 122 EGKGTKKKFFELVLDPAQDWYRWLFVIAMPVLYNWCLLVARACFSDLQRYFVWLVLD 181
Db 120 EGKGTKKKFFELVLDPAQDWYRWLFVIALPVLYNWCLLVARACFSDLQRYFVWLVLD 179
Qy 182 YFSDTVYIADLIRLRTGFEQGLLVKDPKLRDNYIHTLQFKLDVASIIPDTLIVFVG 241
Db 180 YVSDVYIADLIRLRTGFEQGLLVKDPKLRDNYIHTLQFKLDVASIIPDTLIVFVG 239
Qy 242 IHSPEVRNLLHFAFMFEFFRTERTSYPNIRISNLVAVLYLVIHWNACIYVVISKS 301
Db 240 IHNPELRNLLHFAFMFEFFRTERTSYPNIRISNLVAVLYLVIHWNACIYVVISKS 299
Qy 302 IGFGVDTWVYVNTDPEYCYLAREYIYCLYWSLTLTTTIGETPPPVKDEYLVFVDFLI 361
Db 300 IGFGVDTWVYVNTDPEYCYLAREYIYCLYWSLTLTTTIGETPPPVKDEYLVFVDFLI 359
Qy 362 GVLIFATIVGNVSMISNNATRAEFOAKIDAVKHYMPQKYSKMEAKVIRKWFYDLWN 421
Db 360 GVLIFATIVGNVSMISNNATRAEFOAKIDAVKHYMPQKYSKMEAKVIRKWFYDLWN 419
Qy 422 KKTVDREVLKLPKLAKEIAINVHLSLTKKVRIFQDWEAGLLVVLKLRPOVPSGD 481

```

Db 420 KKSVDREVLNPKLPAKRAEIAINVHLSTLKKVRFQDCEAGLLVELVCLKRPQVSPGD 479
 QY 482 YICRGDYGKEMYYIIKEGKLAVVADGVTQVALLSAGSCFGEISILINIKSGKGNRTAN 541
 Db 480 YICRGDYGKEMYYIIKEGKLAVVADGVTQVALLSAGSCFGEISILINIKSGKGNRTAN 539
 QY 542 IRSIGYSDFCLSKDDLMMEATVPAKAVLEERGREILMKVGLLDENEVAASMEVDVQE 601
 Db 540 IRSIGYSDFCLSKDDLMMEATVPAKAVLEERGREILMKVGLLDENEVAASMEVDVQE 599
 QY 602 KLEOLETNDTLYTRFARLLAEYTGAAQKIKQRTIVLETKMKQNHDDYLSGINTPPT 661
 Db 600 KLEOLETNDTLYTRFARLLAEYTGAAQKIKQRTIVLETKMKQNHDDYLSGINTPPT 659
 QY 662 A 662
 Db 660 A 660

RESULT 5

NCBI_CHKID NCBI_CHKID STANDARD; PRT; 735 AA.
 AC Q90805;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cyclic nucleotide-gated channel, cone photoreceptor, alpha subunit
 DE (CNG channel 1) (CNG-1).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archoaureia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]

SEQUENCE FROM N.A.

RX MEDLINE=93264082; PubMed=7684234;
 RA Boenigk W., Altenhofen W., Mueller F., Dose A., Illing M.,
 RA Molday R.S., Kaupp U.B.;
 RT "Rod and cone photoreceptor cells express distinct genes for
 cGMP-gated channels.";
 RL Neuron 10:865-877(1993).
 CC -1- FUNCTION: Visual signal transduction is mediated by a G-protein
 coupled cascade using cGMP as second messenger. This protein can
 be activated by cyclic GMP which leads to an opening of the cation
 channel and thereby causing a depolarization of cone
 photoreceptors.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 (TC 1.A.1.5) family.
 CC -1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.

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 or send an email to license@isb-sib.ch).

DR EMBL; X89598; CAA61757.1; -
 DR PIR; I50630; I50630.
 DR InterPro; IPR000595; cNMP binding.
 DR InterPro; IPR005821; Ion_trans.
 DR Pfam; PF001622; K+channel_pore.
 DR Pfam; PF00520; cNMP binding; 1.
 DR SMART; SM00100; ion_trans; 1.
 DR PROSITE; PS00888; cNMP_BINDING_1; 1.
 DR PROSITE; PS00889; cNMP_BINDING_2; 1.
 DR PROSITE; PS00442; cNMP_BINDING_3; 1.
 KW Ionic channel; Ion transport; cAMP-binding; Transmembrane; Vision;
 KW Multigene family.
 FT DOMAIN 1 210 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM	211	230	H1 (POTENTIAL).
FT DOMAIN	231	243	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	244	262	H2 (POTENTIAL).
FT DOMAIN	263	286	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	287	306	H3 (POTENTIAL).
FT DOMAIN	307	344	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	345	367	H4 (POTENTIAL).
FT DOMAIN	368	419	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	420	439	H5 (POTENTIAL).
FT DOMAIN	440	523	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	524	544	H6 (POTENTIAL).
FT DOMAIN	545	735	CYTOPLASMIC (POTENTIAL).
FT NP_BIND	532	654	CAMP (BY SIMILARITY).
FT BINDING	591	591	CAMP (POTENTIAL).
FT BINDING	606	606	CAMP (POTENTIAL).
FT CARBOHYD	449	449	N-LINKED (GLCNAC..) (POTENTIAL).
SQ SEQUENCE	735 AA;	85031 MW;	A67ADFDD942CFCE CRC64;

Query Match 63.9%; Score 2219.5; DB 1; Length 735;
 Best Local Similarity 59.4%; Pred. No. 1.2e-140;
 Matches 432; Conservative 93; Mismatches 113; Indels 89; Gaps 7;

QY 16	NHNNHPPP	---	SIKANGKDDHRAGS	---	RPOQVAADDDTSPELQRLAEMD	-----	59
Db	5	NTQHSYSGMGLSV	RTTDEIERIENGFI	THSLC	---	EDTSSELQRVISMGRHLSGQT	62
QY 60	TPRGRGGFORIV	LVGVIRDWANKNFR	EEPRPDSFLERFG	PELQTVTTTHQ	---	---	113
Db	63	SPFTGRGAMARL	SFRVSVLSRWATRL	HHEDQRPDSFLER	IRGPELVSSRQNSRFL	122	
QY 114	---	---	---	---	---	---	114
Db	123	GIREQGVGNPWL	ARFNFNNTNEDK	KEKKEKKEKKEK	KDDKDDKDD	182	
QY 115	DKGGKDGEGTK	KKFEFLVD	PAGDWYRFLVIA	MPVLYNCLLVAR	ACPSDLQRYF	174	
Db	183	KKDDKDDKKE	QKKEVFVIDP	SSNNYNNWLTII	IAFYNWMLICR	ACFDELQIDHI	242
QY 175	VWHLVLDYSD	TVIADLIIR	TGFLQGLVKD	PKLRDNYHTL	QPKLDVASIPTD	234	
Db	243	KWLFLDYCD	SIYVDFMFRFT	GFLEQGLLVK	DEKLRDHYTQ	VFKDLVLSLPTD	302
QY 235	LIYFAVGIHS	PEVRENRLH	FAHMRFEF	DETRTSTVPM	IRISNLVILV	IIHWNACI	294
Db	303	LAYLKLGN	PELPELFRN	RLRIARLEFF	FDTRTNYPM	FRIGNLVYLIIHWNACI	362
QY 295	YVVISKISG	VDVTWYPM	ITDPEYGLARE	YIYCLYWS	TLTITTTIGET	PPPVKDEYLF	354
Db	363	YFAISKVIG	FGTDSWYYP	NVSIPYGRLS	SKYIYLSY	WSTLTITTTIGET	422
QY 355	VIFDELIG	VLIFATIV	NGVSGMSI	NNNATPA	EFQAKIDAV	KHYMPFRKYSKDMAKVIKW	414
Db	423	VVIDELVGL	IFATIVNG	VSGMSI	NNNATPA	EFQAKIDAVKHYMPFRKYSKDMAKVIKW	482
QY 415	FQYLTWNKT	VDEREVL	KQIPAKLAE	IAINVHLS	TLKKVRIF	QDWEAGLLVELVCLKRP	474
Db	483	FQYLTWNKT	VDEREVL	KQIPAKLAE	IAINVHLS	TLKKVRIFQDWEAGLLVELVCLKRP	542
QY 475	QVFSFGDY	ICRKGDIG	KEMYYII	KEGKLAV	ADGVTQVALL	SAGSCFGEISILINIKSGK	534
Db	543	TVFSPGDY	ICKGDI	GREMYII	KEGKLAV	ADGVTQVALLSAGSCFGEISILINIKSGK	602
QY 535	GNRRTANIR	SGYSD	FLCLSKDD	LMMEATV	PAKAVLEER	GREILMKVGLLDENEVAAS	594
Db	603	GNRRTANIR	SGYSD	FLCLSKDD	LMMEATV	PAKAVLEERGREILMKVGLLDENEVAAS	662
QY 595	ME	-VDVQEK	LEOLET	NMDTLY	TRFARLLAE	YTGAAQKIKQRTIVLETKMKQNHDDYLSG	653
Db	663	ADPKDLE	KIDRL	ETALD	TLQTRFAR	LLAEYSSSQKQKRLARVETRVKK	717
QY 654	GINTPEP	660					
Db	718	SLSVGP	724				

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RESULT 6
CNG3_MOUSE
ID CNG3_MOUSE STANDARD; PRT; 631 AA.
AC Q9JZ8; Q9WV01;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha 3)
DE (CNG-3) (CNG3) (Cyclic nucleotide-gated channel alpha 3) (Cone
DE photoreceptor cGMP-gated channel alpha subunit).
GN CNGA3 OR CNGB3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Retina;
RX MEDLINE=20273944; PubMed=10813773;
RA Harano A.A., Hack I., Waessle H., Duvoisin R.M.;
RT "Cloning and immunocytochemical localization of a cyclic nucleotide-
RT gated channel alpha-subunit to all cone photoreceptors in the mouse
RT retina.";
RL J. Comp. Neurol. 421:80-94 (2000).
RN [2]
RP SEQUENCE OF 95-631 FROM N.A.
RC STRAIN=129/Sv;
RX MEDLINE=99307448; PubMed=10377453;
RA Biel M., Seeliger M., Pfeiffer A., Kohler K., Gerstner A., Ludwig A.,
RA Jaisle G., Fauser S., Zrenner E., Hofmann F.;
RT "Selective loss of cone function in mice lacking the cyclic
RT nucleotide-gated channel CNG3.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:7553-7557 (1999).
CC -1- FUNCTION: Visual signal transduction is mediated by a G-protein
CC coupled cascade using cGMP as second messenger. This protein can
CC be activated by cyclic GMP which leads to an opening of the cation
CC channel and thereby causing a depolarization of cone
CC photoreceptors.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Prominently expressed in retina.
CC -1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
CC (TC 1.A.1.5) family.
CC -1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC
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CC
DR EMBL; AJ243933; CAB89685.1; -.
DR EMBL; AJ238239; CAB42891.1; -.
DR EMBL; AJ238240; CAB42891.1; JOINED.
DR EMBL; AJ238241; CAB42891.1; JOINED.
DR MGD; MGI:1341818; Cng3a3.
DR GO; GO:0005223; F:intracellular cyclic nucleotide activated c...; IPI.
DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel_pore.
DR Pfam; PF00027; cNMP binding; 1.
DR Pfam; PF00520; ion trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP BINDING 1; 1.
DR PROSITE; PS00889; cNMP BINDING 2; 1.
DR PROSITE; PS0042; cNMP BINDING 3; 1.
DR KW Multigene family; Vision.
FT TRANSMEM 112 133 POTENTIAL.
FT TRANSMEM 244 264 POTENTIAL.

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FT TRANSMEM 320 340 POTENTIAL.
FT NP_BIND 423 546 CAMP.
FT BINDING 490 505 CAMP (POTENTIAL).
FT BINDING 505 505 CAMP (POTENTIAL).
FT CONFLICT 110 110 C -> Y (IN REF. 2).
FT CONFLICT 157 157 L -> V (IN REF. 2).
SQ SEQUENCE 631 AA; 72641 MW; 4FA8CD3B9AA3FE6C CRC64;

Query Match 61.9%; Score 2151.5; DB 1; Length 631;
Best Local Similarity 66.8%; Pred. No. 3.5e-136;
Matches 411; Conservative 85; Mismatches 94; Indels 25; Gaps 5;

QY 57 EMDTPRRGRGGFORIVLVGVIRDWANKFNPREPRPDSFLERPRGDELQVTHQ----- 112
Db 24 DLQHVENG--RVSELIISIRAWASHLHDEQDPDSFLDRPHSELKEVSTRESNAQ 80
QY 113 ---GDDKGGKGGKGTFFELFVLDPAQDWYRWFVIAFVLYVNCWLLVARACFSDL 169
Db 81 PNPGEQKPPDGGEG---RKEEPIVVDPSNIIYCRWLTALTAIFVYVNCWLLVCRACFDEL 136
QY 170 QRVNFFVVLVLDYFSDTVIADLIIRLTGFLQGLLVDPKPKLRDNYIHTLOFKLDVAS 229
Db 137 QSHLTLWGLVDYSADVLYVLDVRAARTGFLQGLVMDTKLWKHYTKTLHFKLDIIS 196
QY 230 IIPDLIYFAVGHSPEVRFNRLHFARMPFEDRTETSYENIPIRISNLVLYIIVIH 289
Db 197 LIPTDLAYLKLGVNYPELFRNLLKFSRLEFEDRTETRYPNVFRIGNLVLYIIVIH 256
QY 290 WNAIYVYVSKISGFGVDTWVYVNIPTDPEYGLAREYIYCLXWSTLTLTIGETPPVKD 349
Db 257 WNAIYFAISKETGFGTDSWYVNTSKPEYARLSKVIYSLYWSTLTLTIGETPPVKD 316
QY 350 EYLFVLPDPLIGLVLFATVGVNCSMISMNATRAEFOAKIDAVKHYNQFRKVSXDEA 409
Db 317 EYLFVLPDPLIGLVLFATVGVNCSMISMNAPVEFOAKIDSVKQYQFRKVTXDEL 376
QY 410 KVIMFDYLVMTNKTVDEREVLKPLAKLRAEIAINHLSTLTKVRI FODWEAGLLELV 469
Db 377 RVIRFDYLVNKRKTVDKEVLKPLKALINHLDTLKKVRI FODCEAGLLELV 436
QY 470 LKLRQVSPGYI CKGDIGEMWIIKGLVAVVADGVTQVALISAGSCFEISILNI 529
Db 437 LKLRQVSPGYI CKGDIGEMWIIKGLVAVVADGVTQVALISAGSCFEISILNI 496
QY 530 KGSKNMNRRTANIRSLGYSDFCLSKDDLMEAVTEAPDAKVLBERGRIIMKMLDEN 589
Db 497 KGSKNMNRRTANIRSLGYSDFCLSKDDLMEAVTEAPDAKVLBERGRIIMKMLDEN 556
QY 590 EVAASMEV-DVQEKLEQLETNMDTLTYRFAIRLAETGAQKQKQITVLETKM----- 642
Db 557 LVAAVDTVDVEKVEYLESSLDILQTRFARLLAAYSASQMKLQRLTLESQMMNRCCG 616
QY 643 ----KQNEHEDDVLSD 653
Db 617 FSPDRENSDASKTD 631

RESULT 7
CNG3_BOVIN
ID CNG3_BOVIN STANDARD; PRT; 706 AA.
AC Q29441;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha 3)
DE (CNG-3) (CNG3) (Cyclic nucleotide-gated channel alpha 3) (Cone
DE photoreceptor cGMP-gated channel alpha subunit).
GN CNGA3 OR CNGB3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;

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RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Testis;
RA  MEDLINE=94211295; PubMed=7512693;
RA  Weyand I., Godde M., Frings S., Weiner J., Mueller F., Altenhofen W.,
RA  Hat H., Kaupp U.B.;
RT  "Cloning and functional expression of a cyclic-nucleotide-gated
RL  channel from mammalian sperm.";
RL  Nature 368:859-863(1994).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Kidney;
RX  MEDLINE=94224768; PubMed=8170936;
RA  Biel M., Zong X., Distler M., Bosse E., Klugbauer N., Murakami M.,
RA  Flockerzi V., Hofmann F.;
RT  "Another member of the cyclic nucleotide-gated channel family,
RT  expressed in testis, kidney, and heart.";
RL  Proc. Natl. Acad. Sci. U.S.A. 91:3505-3509(1994).
CC  -!- FUNCTION: Could be responsible for cGMP-induced calcium entry in
CC  cells other than sensory cells. Might be involved in chemotaxis of
CC  sperm.
CC  -!- SUBUNIT: Forms functional heterooligomeric channels with CNG4 in
CC  vitro.
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -!- TISSUE SPECIFICITY: Testis, kidney, retinal cone and heart.
CC  -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
CC  (TC 1.A.1.5) family.
CC  -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X89600; CAA61759.1; -;
DR  EMBL; X76485; CAA54023.1; -;
DR  PIR; A55251; A55251.
DR  InterPro; IPR000595; CNMP binding.
DR  InterPro; IPR005821; Ion Trans.
DR  InterPro; IPR001622; K-channel_pore.
DR  Pfam; PF00027; cnmp_binding; 1.
DR  Pfam; PF00520; ion_trans; 1.
DR  SMART; SM00100; CNMP; 1.
DR  PROSITE; PS00888; CNMP_BINDING_1; 1.
DR  PROSITE; PS00889; CNMP_BINDING_2; 1.
DR  PROSITE; PS50042; CNMP_BINDING_3; 1.
KW  Ionic channel; Ion transport; cAMP-binding; Transmembrane;
KW  Multigene family; Vision.
FT  TRANSMEM 186 206 POTENTIAL.
FT  TRANSMEM 322 342 POTENTIAL.
FT  TRANSMEM 398 418 POTENTIAL.
FT  NP_BIND 501 624 CAMP.
FT  BINDING 568 568 CAMP (POTENTIAL).
FT  BINDING 583 583 CAMP (POTENTIAL).
SQ  SEQUENCE 706 AA; 81132 MW; F4990DCD29B56239 CRC64;
Query Match
Best Local Similarity 61.6%; Score 2140; DB 1; Length 706;
Matches 419; Conservative 94; Mismatches 119; Indels 62; Gaps 7;
QY 11 SSPANNHHPPPSKANGKD-DHRRAGRPQSVAAADDTSPELOFLAEMDTFRGRG--- 66
DB 9 SHPTRTH-----PSVRTMDRLDCIENGLSRTHLPCEITSSELQEGIAMET--RGLAESR 61
QY 67 -----GFORIVLGVIRWANKNFREPRDPDSFLERPGPELOQVTHQG----- 113
DB 62 QSSFTSQGFTRLSRLIISLRAWSAHLHQEQRPDSFLERFPGAFLQVSSRESHVQPNV 121
QY 114 -----DDKGGKDGE-----GKGTKKKFLFVLD 136

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DB 122 GSQPPDGRSAWPLARNNTNNTCNNSEKODKAKKEKEKEKKEKPKKEKKKSDVVMVD 181
QY 137 PAGDWYRWLFVFIAMPVLYNWCLLVARACFSDLGSRNVFVWVLDYSDTYVIAIDLIRL 196
DB 182 PSSNNYHMLTVIAPVYFNWCLLVCRACDFDESEHMLMLWLVLDYSDIILYGMMLVRA 241
QY 197 RTGFEQGLLVKPKLRDNYIHTLOPKLDVASIIPITDLIYFAVGHSPEVRFNRLHFA 256
DB 242 RTGFEQGLVMDASRLWKHYTQTLHFKLDVLSVPTDLAYFKLGMVPELRENLKLA 301
QY 257 RMPEFFDRTETRTSYFNI FRISNLVILVILIIHNACIYVVISKISIGGVDTWTPNITD 316
DB 302 RLFEFFDRTETRTNYPNMFRI GNVLVYLIIHNACIYFAISKFIQFGTDSWYYPNVSN 361
QY 317 PEYGLAREYICLYWSTLTTLTIGETPPPPVKDDEYLFIQFDFLIGLVI FATI VGNV GSM 376
DB 362 PEYGLRSKYIYSLYNSTLTTLTIGETPPPPVKDDEYLFIQFDFLIGLVI FATI VGNV GSM 421
QY 377 ISNNNATRAEFQAKIDAVKHYMQPRKVKDKMEAKVIKWFDFYLTNKKTVDBEREVLKMLPA 436
DB 422 ISNNNASRAEFQAKIDSIKYMQPRKVKDKLETRVIRWFDYLMANKKTVDKEVLKSLPD 481
QY 437 KLRAEIAINVHLSLTKVRI FQDWEAGLLVELVLKLPQVFPSPGDIYCRKGDIGKEMVII 496
DB 482 KLRAEIAINVHLDTRKVRIFQDCEAGLLVELVLKLPQVFPSPGDIYCRKGDIGREMYII 541
QY 497 KEGKLAVVADDGVTOYALLSAGSCFGEISILINIKSGSKGNRRRTANIRSLGYSDFLCLSKD 556
DB 542 KEGKLAVVAEDGITQFVVLGDSYFGEISILINIKSGSKGNRRRTANIRSLGYSDFLCLSKD 601
QY 557 DLMEAVTPEADPAKVLFEERREILMKMGLLDENEVAASME-VDVQEKLEQLETNMDTYT 615
DB 602 DLMEALTEYPEAKKALEEKGRQILMKONLIDELAKAGADPKDTEEKVEHLETSLSLQ 661
QY 616 RFARLLIARYGAQOKLQKRTVLTETKMKQNHEDD 649
DB 662 RFARLLAEYNATOMKVKQRLESQVQKMGILPPD 695
RESULT 8
CN3 HUMAN
ID -CN3_HUMAN STANDARD; PRT; 694 AA.
AC Q16281; Q9UP64;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha 3)
DE (CNG-3) (CNG3) (Cyclic nucleotide gated channel alpha 3) (Cone
DE photoreceptor cGMP-gated channel alpha subunit).
GN CN3 OR CN3G3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98176633; PubMed=9517456;
RA Wessinger B., Muller F., Weyand I., Schuffenhauer S., Thanos S.,
RA Kaupp U.B., Zrenner E.;
RT "Cloning, chromosomal localization and functional expression of the
RT gene encoding the alpha-subunit of the cGMP-gated channel in human
RT cone photoreceptors.";
RL Eur. J. Neurosci. 9:2512-2521(1997).
RN [2]
RP SEQUENCE OF 320-580 FROM N.A.
RX MEDLINE=95175019; PubMed=7532614;
RA Distler M., Biel M., Flockerzi V., Hofmann F.;
RT "Expression of cyclic nucleotide-gated cation channels in non-sensory
RT tissues and cells.";
RL Neuropharmacology 33:1275-1282(1994).
RN [3]
RP VARIANTS RMCH, AND VARIANT MET-153.
RX MEDLINE=98324775; PubMed=9662398;

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RA Kohl S., Marx T., Giddings I., Jaegle H., Jacobson S.G.,
 RA Apfelstedt-Syllia E., Zrenner E., Sharpe L.T., Wissing B.,
 RT "Total colourblindness is caused by mutations in the gene encoding the
 RT alpha-subunit of the cone photoreceptor cGMP-gated cation channel.";
 RL Nat. Genet. 19:257-259 (1998).
 CC -!- FUNCTION: Visual signal transduction is mediated by a G-protein
 CC coupled cascade using cGMP as second messenger. This protein can
 CC be activated by cyclic GMP which leads to an opening of the cation
 CC channel and thereby causing a depolarization of cone
 CC photoreceptors.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Prominently expressed in retina.
 CC -!- DISEASE: Defects in CNGA3 are a cause of rod monochromacy (RMCH)
 CC [MIM:216900]; also known as total colorblindness or achromatopsia.
 CC RMCH is an autosomal recessively inherited condition.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 CC (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC -!- DATABASE: NAMES=Mutations of the CNGA3 gene;
 CC NOTE=Retina International's Scientific Newsletter;
 CC WWW="http://www.retina-international.com/sci-news/cnga3mut.htm".
 CC -----
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 CC -----
 DR EMBL; A0665314; AAC17440.1; -.
 DR EMBL; S76069; AAD14208.1; -.
 DR PIR; I78560; I78560.
 DR Genew; HGNC:2150; CNGA3.
 DR MIM; 600053; -.
 DR MIM; 216900; -.
 DR GO; GO:0015276; F:ligand-gated ion channel activity; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR GO; GO:0006810; P:transport; TAS.
 DR GO; GO:0007601; P:vision; TAS.
 DR InterPro; IPR000595; cNMP binding.
 DR InterPro; IPR005821; Ion Trans.
 DR InterPro; IPR001622; K-channel pore.
 DR Pfam; PF00027; cNMP binding; 1.
 DR Pfam; PF00520; Ion trans; 1.
 DR SMART; SM00100; cNMP; 1.
 DR PROSITE; PS00888; CNMP BINDING_1; 1.
 DR PROSITE; PS00889; CNMP BINDING_2; 1.
 DR PROSITE; PS00042; CNMP BINDING_3; 1.
 KW Ionic channel; Ion transport; cAMP-binding; Transmembrane;
 KW Multigene family; Vision; Disease mutation; Polymorphism.
 FT TRANSMEM 171 192
 FT TRANSHEM 305 325 POTENTIAL.
 FT TRANSHEM 378 397 POTENTIAL.
 FT NP_BIND 482 605 CAMP.
 FT BINDING 549 549 CAMP (POTENTIAL).
 FT BINDING 564 564 CAMP (POTENTIAL).
 FT VARIANT 153 153 T -> M.
 FT VARIANT 163 163 /FTid=VAR_010902.
 FT P -> L (in RMCH).
 FT VARIANT 283 283 /FTid=VAR_010903.
 FT R -> Q (in RMCH).
 FT VARIANT 283 283 /FTid=VAR_010904.
 FT R -> W (in RMCH).
 FT VARIANT 291 291 /FTid=VAR_010905.
 FT T -> R (in RMCH).
 FT VARIANT 410 410 /FTid=VAR_010906.
 FT R -> W (in RMCH).
 FT VARIANT 529 529 /FTid=VAR_010910.
 FT V -> M (in RMCH).
 FT VARIANT 547 547 /FTid=VAR_010907.
 FT F -> L (in RMCH).
 FT /FTid=VAR_010908.

FT VARIANT 557 557 G -> R (in RMCH).
 FT /FTid=VAR_010909.
 SQ SEQUENCE 694 AA; 78838 MW; AE00BAEE76D070A0 CRC64;
 Query Match 61.6%; Score 2139; DB 1; Length 694;
 Best Local Similarity 61.5%; Pred. No. 2.7e-135;
 Matches 429; Conservative 93; Mismatches 129; Indels 46; Gaps 10;
 QY 5 KNGVSSPANNHHPPIKANGKDDHAG---SRQSVAAADDTSPELQRLAEMDT- 60
 DB 3 KINTQSHPSRTH-----LKVTSRDNLNRAENGSLRAHS--SSETSVLQPGIAMETR 55
 QY 61 --PRGRG-----GFQIRVLRVGVIRDMANKFREPEPDSFLERFGPELQTVTTHQ 113
 DB 56 GLADSSQGSFTQGIARLSRLIFLLRWAARVHHQDQGFDPDRFRGAELKEVSSQS 115
 QY 114 D-----DKG-----GKDGEGKTKKPELFLVDLADGWIYRWLFV 148
 DB 116 NAAQNVGSQBPADRGSAWPLAKONTNTSNTEEKTKK-DAIVDPSSNLYRWLTA 174
 QY 149 IAMPVLNWCLLVACAFSDLQNTFVVMVLVDYFSDTVYIADLIIRLTGFLQGLLVK 208
 DB 175 IALPFYNYLLICACFDELQSEYLMMLVDYSADVLVLDLVRARTGLEQLMVS 234
 QY 209 DPKKLRDNIHTLQFKLDVASIIPDILYFVAGIHSPEVRFNRLHFAFMFFDRTETR 268
 DB 235 DTNRLWQHYKTTTQFKLDVLSVPTDLVYLVGTNYPEVRFNRLKFSRLFFDRTETR 294
 QY 269 TSYPNIFRISNLVILVLIHWNACIYVYSKISGRVDVTWYVYVNTDPEYGLAREYIY 328
 DB 295 TNPNNFRIGNLVLYLIIHWNACIYFAISKIFGTDSDWYVYVNTDPEYGLAREYIY 354
 QY 329 CLYWSLTTLTIGETPPPVKDBEYLFVDFDLIGLVLFATIVGNVGSMSNMNATRAEFQ 388
 DB 355 SLYWSLTTLTIGETPPPVKDBEYLFVVDVFLVGLVLFATIVGNVGSMSNMNATRAEFQ 414
 QY 389 AKIDAVKHMOPRKYSKOMEAKVWFYLVNWKTVDERVLKNIPAKRAEIAINVHL 448
 DB 415 AKIDSIKQYMQFRKVTQLETRVIRWFDYLVANKTVDEKVLKSLPDKLAEIAINVHL 474
 QY 449 STLKVRIFQDWEAGLVLLKLRPQVPSPGDYICRKGDIGKEMVIIKEGLAVVADDG 508
 DB 475 DTLKVRIFQDCEAGLVLLKLRPQVPSPGDYICRKGDIGKEMVIIKEGLAVVADDG 534
 QY 509 VTQYALLSAGSCFGEISILNIKSGMGNRTANIRSLGYSDFLCLSKDDLMEAVTAPDA 568
 DB 535 VTQFVVLSDGYPGEISILNIKSGMGNRTANIRSGYSDFLCLSKDDLMEALTEYPEA 594
 QY 569 KKVLEERGRIILMKGLLDENEVAASME-VDYQEKLEQLETNMDTLYTFARLLAEYVGA 627
 DB 595 KKALEEKGRQILMKONLIDELARAGADPKDLEEKVEQLGSSLDLTQTRPARLLBYNAT 654
 QY 628 QQKLRITVLETKMKQNEHDDYLSDGINTPEPTAAE 664
 DB 655 QMKMKQRLSQLESQVK-GGGDKPLADGEVPGDATKTE 690
 RESULT 9
 ID_CNG ICTPU STANDARD; PRT; 682 AA.
 AC P55934;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cyclic-nucleotide-gated cation channel.
 OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 OC Ictaluridae; Ictalurus.
 CX NCBI_TaxID=7998;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory neuroepithelium;

DR InterPro; IPR001622; K+channel_pore.
 DR Pfam; PF00027; cNMP binding; 1.
 DR Pfam; PF00520; ion trans; 1.
 DR SMART; SM00100; cNMP; 1.
 DR PROSITE; PS00888; cNMP_BINDING_1; 1.
 DR PROSITE; PS00889; cNMP_BINDING_2; 1.
 DR PROSITE; PS00442; cNMP_BINDING_3; 1.
 KW Ionic channel; Ion transport; CAMP-binding; Transmembrane; Vision;
 KW Multigene family.
 KW DOMAIN 1 117 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 118 137 H1 (POTENTIAL).
 FT DOMAIN 138 150 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 151 169 H2 (POTENTIAL).
 FT DOMAIN 170 193 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 194 213 H3 (POTENTIAL).
 FT DOMAIN 214 251 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 252 274 H4 (POTENTIAL).
 FT DOMAIN 275 326 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 327 346 H5 (POTENTIAL).
 FT DOMAIN 347 430 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 431 451 H6 (POTENTIAL).
 FT DOMAIN 452 645 CYTOPLASMIC (POTENTIAL).
 FT NP_BIND 439 561 CAMP (BY SIMILARITY).
 FT BINDING 498 498 CAMP (POTENTIAL).
 FT BINDING 513 513 CAMP (POTENTIAL).
 FT CARBOHYD 377 377 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 645 AA; 989DS15F61AC7D31 CRC64;
 Query Match 59.5%; Score 2067; DB 1; Length 645;
 Best Local Similarity 62.9%; Pred. No. 1.6e-130; Indels 38; Gaps 6;
 Matches 406; Conservative 78; Mismatches 123;
 QY 19 HPPPSKANGKDDHAGSPQSVAAADDTSPELQRLAEMDTPRRGRGFGQFQIRVLVGV 78
 DB 9 HHSHP11-----PSVVVDTSPPGL-----IEKGENRRARQWYLPQAF 47
 QY 79 -----RDWANKNPREBEPDPSFLERFQPELQVTTHQGDGKGDGEGKTK 128
 DB 48 AQYNNNNNSNKDEKKKKKKSENKDKGERQKNEKKKKNKDK----KKGEEK 103
 QY 129 KFLFVLDPADGWYRWLFVIAWVLYNWCLLVARCFSDLORNYFVVLVLDVFSITVY 188
 DB 104 KDLFIIDPAGNYNWFCTMPVYNWNTMIARACFDELQNDLAWFIVDVSVIY 163
 QY 189 IADLIIRLTGFLQGLVQKPKLRDNYHTLQFLDVAISIITDLYFAVGHSEVR 248
 DB 164 IADMVFRTRTGLYEQGLLVKEEQKLKQYKSSIQFLDLSIITDLYLFLKGLNYPFLR 223
 QY 249 ENRLHFAWPEFFDRTRTSYENIFRISNLVLYLVIHWNACIYVVISKSTGFQVDT 308
 DB 224 INRLRVARMEFFORTETRTNYNIFRISNLVLYLVIHWNACVYVISKAIQFGADT 283
 QY 309 WVPNTIDPEGYLAREYICLYWSTLTITIGETPPPKDEEYLVIFDPLGLVIFAT 368
 DB 284 WYVINTSHPEARLTRKYVSLYSLWSTLTITIGETPPVRDSEYFVVDVFLVGLIFAT 343
 QY 369 IVGVNISMNNATRAEFQAKIDAVKHYMFRKVKDMEAKVWKFDYLMWNKKTVDYR 428
 DB 344 IVGVNISMNNARAARAEFQAKIDAIQYHFRNVSKDMKRVIKWFDYLMWNKKAVDYR 403
 QY 429 EVLKNLPKLAETAINVHLSLTKKVRIFQDWEAGLLVVLKLRPQVFPDGYICRKG 488
 DB 404 EVLYLPKLAETAINVHLSLTKKVRIFADCEAGLLVVLKLRPQVFPDGYICRKG 463
 QY 489 IGKMYIIEKGLAVADDGVTVQVALLSAGSCFGEISITNKGKMGNRRTANRSIGYS 548
 DB 464 IGRMYIIEKGLAVADDGVTVQVLLSDGYSFGEISITNKGKMGNRRTANRSIGYS 523
 QY 549 DLFCISKDDLMEAVTEAPDAKKVLEERGREILMKMGLLDENEVA--ASMEYDVQEKLEQ 606
 DB 524 DLFCISKDDLMEALTEYPAKAMLEEKKGKILMKDGLLD-IEVANLGSDPKDLEKAYM 582
 QY 607 ETNMDTLTFRALLAEYTGAAQQLKQRTVLETYKMKQNHDDYL 651

Db 583 EGSMDRLQTKFARLLAEYDAAQQLKRLTQIEKILKPVMEQEF 627
 RESULT 11
 CNGL_BOVIN STANDARD; PRT; 690 AA.
 ID AC Q00134;
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE cNMP-gated cation channel alpha 1 (CNG channel alpha 1) (CNG-1) (CNG1)
 DE (Cyclic nucleotide-gated channel alpha 1) (Cyclic nucleotide-gated
 DE channel, photoreceptor) (Cyclic-nucleotide-gated cation channel 1)
 DE (Rod photoreceptor cGMP-gated channel alpha subunit).
 GN NGAL OR CNG1 OR CNGC.
 OS Bos taurus (Bovine).
 OC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 CX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=retinal rod cell;
 RX MEDLINE=90098076; PubMed=2481236;
 RA Kaupp U.B., Nildome T., Tanabe T., Terada S., Boenigk W.,
 RA Stuehmer W., Cook N.J., Kangawa K., Matsuo H., Hirose T., Miyata T.,
 RA Numa S.;
 RT "Primary structure and functional expression from complementary DNA
 RT of the rod photoreceptor cyclic GMP-gated channel.";
 RL Nature 342:762-766(1989).
 RN [2]
 RP 3D-STRUCTURE MODELING OF 485-610.
 RX MEDLINE=92256398; PubMed=1316156;
 RA Kumar V.D., Weber I.T.;
 RT "Molecular model of the cyclic GMP-binding domain of the cyclic GMP-
 RT gated ion channel.";
 RL Biochemistry 31:4643-4649(1992).
 RN [3]
 RP TOPOLOGY.
 RX MEDLINE=95365381; PubMed=7543681;
 RA Henn D.K., Baumann A., Kaupp U.B.;
 RT "Probing the transmembrane topology of cyclic nucleotide-gated ion
 RT channels with a gene fusion approach.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7425-7429(1995).
 RN [4]
 RP TOPOLOGY.
 RX MEDLINE=92112723; PubMed=1370452;
 RA Wohlfart P., Haase W., Molday R.S., Cook N.J.;
 RT "Antibodies against synthetic peptides used to determine the topology
 RT and site of glycosylation of the cGMP-gated channel from bovine rod
 RT photoreceptors.";
 RL J. Biol. Chem. 267:644-648(1992).
 CC -1- FUNCTION: Visual signal transduction is mediated by a G-protein
 CC coupled cascade using cGMP as second messenger. This protein can
 CC be activated by cGMP which leads to an opening of the cation
 CC channel and thereby causing a depolarization of rod
 CC photoreceptors.
 CC -1- SUBUNIT: Homotetramer or higher oligomer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Rod cells in the retina.
 CC -1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 CC (TC 1.A.1.5) family.
 CC -1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC -----
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CC WWW="http://www.retina-international.com/sci-news/cngalmut.htm".
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CC -----
DR EMBL; M64741; AAAS2010.1; AUT_INIT.
DR EMBL; S42457; AAB22778.1; -.
DR EMBL; S76062; AAD14206.1; -.
DR PIR; A42161; A42161.
DR Genew; HGNC:2148; CNGA1.
DR MIM; 123825; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0006810; P:transport; TAS.
DR GO; GO:0007601; P:vision; TAS.
DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR005821; Ion Trans.
DR Pfam; PF00027; cNMP_binding; 1.
DR SMART; SM00520; Ion_Trans; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; 1.
DR PROSITE; PS00889; cNMP_BINDING_2; 1.
DR PROSITE; PS50042; cNMP_BINDING_3; 1.
KW Tonic channel; Ion transport; cNMP-binding; Transmembrane;
KW Multigene family; Vision; Disease mutation; Polymorphism;
KW Retinitis pigmentosa.
FT DOMAIN 1 160
FT TRANSEM 161 181
FT DOMAIN 182 194
FT TRANSEM 195 213
FT DOMAIN 214 237
FT TRANSEM 238 257
FT DOMAIN 258 295
FT TRANSEM 296 318
FT DOMAIN 319 370
FT TRANSEM 371 390
FT DOMAIN 391 474
FT TRANSEM 475 495
FT DOMAIN 496 686
FT NP BIND 483 605
FT BINDING 542 542
FT BINDING 557 557
FT CARBOHYD 421 421
FT VARIANT 28 28
FT VARIANT 114 114
FT VARIANT 316 316
FT CONFLICT 46 46
FT CONFLICT 85 85
FT CONFLICT 146 147
FT CONFLICT 539 539
FT CONFLICT 677 678
FT SEQUENCE 686 AA; 79126 MW; B5200D216FC97AF6 CRC64;
Query Match 50.5%; Score 2034; DB 1; Length 686;
Best local similarity 61.4%; Pred. No. 2.7e-128;
Matches 403; Conservative 88; Mismatches 135; Indels 30; Gaps 5;
QY 23 PSIKANGKDDHGRAGRQPSVAADDTSPELQRLAEMDTPRRGRGF-----ORI 71
DB 21 PDIE---KEIKRMENGACSFSDDDSDASTSESENEHP-HARGSFYSKLRKGGPSQRE 76
QY 72 VRLVGIVR-----DWANKFRDEEPRPDSFLERFRGPELQTVTHQGDDKG 117
DB 77 QYLFGAIFALFNWNSNKKQDEPEKKKKKKKKSKSDKKNKNDPEKKKKKKKKKK 136

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QY 118 GKDGGKGTGKKKFLFVLDPPAGDWYRMLFVIAMFVLNWNCLLVARACFSQIQRNVFVW 177
DB 137 EKSXDKKEEKEVVVIDPSGNTYNNMFCITLFWNNTWVIARACFDELQSDYLEW 196
QY 178 LVLDFSTVYADLIILRLTGFLBQGLLVDPKPKLRDNYIHTLQFKLDVASILPTDLY 237
DB 197 LLDVSDIVLIDMFVTRTGYLQGLLVKELKLNKYKSNLQFKLDVLSLIPDLY 256
QY 238 FAVGHTSPVRNRLHFMPEFFDRTETRTSYENIFRISNLVLYLVIHWNACIYV 297
DB 257 FKLGNYPBIRLNLRLRSRMFEFFQRTETRYNIFRISNLVYIVIIHWNACVYS 316
QY 298 ISKISGFGVDWVYNNITDPEGYLAREYIYCLYWSLTTLTIGTTPPVKDEYLFVIF 357
DB 317 ISKALGFGNDTWVYPDINDPFRGLARKYVSYLSYWSLTTLTIGTTPPVSEYFVVV 376
QY 358 DFLIGVLIFATVGNVSMISNNNATRAEFAKIDAVKHVMOPRVKSKDMEAKVIKWDY 417
DB 377 DFLIGVLIFATVGNIGSMISNNNAARAEFAQIDAIQYMHFRNVSKDMEKRVIKWDY 436
QY 418 LWTNKKTVDEREVLNKLPAKRAEIAINVHLSTLKKVRFQDWEAGLLVVLKLRPQVF 477
DB 437 LWTNKKTVDEKEVLKPLDKLPAEIAINVHLDTLKKVRIFADCEAGLLVVLKLPQVY 496
QY 478 SPGDYICRKGDIGKEMYIIKEGLAVADDGVTQVALLSAGSCFGEISILNKGSKGNR 537
DB 497 SPGDYICKKGDIGREMYIIKEGLAVADDGVTQFVVLSDGSYFGEISILNKGSKAGR 556
QY 538 RTANIRSLGYSDFCLSKDGLMEAVTEAPDAKVLLEERGRELKMKGLDENEV-AASME 596
DB 557 RTANIKSIGYDLFCLSKDGLMEALTEYDPAKMLFEKQKILMKDGLDLNANAGSDP 616
QY 597 VDVQEKLEQLETNMDTLTYFRARLLAEYTGAAQKLRITVLETKMKQNHEDDYL 652
DB 617 KDLKVKVTEMGSDVLLQTRFARILAEVSMQKLRITVLETKMKPLIDTFESS 672
RESULT 13
CNGI_RAT
ID_CNGI_RAT STANDARD; PRT; 683 AA.
AC O6297; O08659;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-NOV-2004 (Rel. 43, Last annotation update)
DE cNMP-gated cation channel alpha 1 (CNG channel alpha 1) (CNG-1) (CNGI)
DE (Cyclic nucleotide-gated channel alpha 1) (Cyclic nucleotide-gated
DE channel, photoreceptor) (Cyclic-nucleotide-gated cation channel 1)
DE (Rod photoreceptor cNMP-gated channel alpha subunit).
GN CNGA1 OR CNCG1 OR CNCG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Barnstable C.J., Wei J.Y.;
RL Submitted (C.N.J., Wei J.Y.) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97287732; PubMed=9142860;
RA Ding C., Potter E.D., Qiu W., Coon S.L., Levine M.A., Guggino S.E.;
RT "Cloning and widespread distribution of the rat rod-type cyclic
RT nucleotide-gated cation channel."
RL Am. J. Physiol. 272:G1335-G1344(1997).
RN [3]
RP SEQUENCE OF 521-693 FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97197878; PubMed=9045728;
RA Bradley J., Zhang Y., Bakin R., Lester H.A., Ronnett G.V., Zinn K.;
RT "Functional expression of the heteromeric 'olfactory' cyclic
RT nucleotide-gated channel in the hippocampus: a potential effector of
RT synaptic plasticity in brain neurons."

```


CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 CC (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X99914; CAAG8186.1; -;
 CC EMBL; U83905; AAB61707.1; -;
 CC PIR; JC6509; JG6509.
 CC InterPro; IPR000595; cNMP_binding.
 CC InterPro; IPR005821; Ion_trans.
 CC InterPro; IPR001622; K+channel_pore.
 CC Pfam; PF00027; cNMP_binding; 1.
 CC Pfam; PF00520; ion_trans; 1.
 CC SMART; SM00100; cNMP; 1.
 CC PROSITE; PS00868; cNMP_BINDING_1; 1.
 CC PROSITE; PS00889; cNMP_BINDING_2; 1.
 CC PROSITE; PS50042; cNMP_BINDING_3; 1.
 CC Ionic channel; Ion transport; cGMP-binding; Transmembrane;
 CC Multigene family; Vision.
 CC DOMAIN 1 163 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 164 184 H1 (POTENTIAL).
 CC DOMAIN 185 197 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 198 216 H2 (POTENTIAL).
 CC DOMAIN 217 240 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 241 260 H3 (POTENTIAL).
 CC DOMAIN 261 298 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 299 321 H4 (POTENTIAL).
 CC DOMAIN 322 373 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 374 393 H5 (POTENTIAL).
 CC DOMAIN 394 477 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 478 498 H6 (POTENTIAL).
 CC DOMAIN 499 691 CYTOPLASMIC (POTENTIAL).
 CC NP_BIND 486 608 CGMP (POTENTIAL).
 CC BINDING 545 560 CGMP (POTENTIAL).
 CC BINDING 560 560 CGMP (POTENTIAL).
 CC CARBOHYD 424 424 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 691 AA; 80251 MW; 0775CAA42F065275 CRC64;
 Query Match 58.1%; Score 2017.5; DB 1; Length 691;
 Best Local Similarity 61.3%; Pred. No. 3.5e-127; Indels 31; Gaps 7;
 Matches 398; Conservative 94; Mismatches 126;
 23 PSIKANGKDDHRRAGSRPQSVAAAD---DDTSPQLQRLAEMDTPR-----RGRGGFOR 70
 21 PDIE--KEIRRMENGARSSFDSDGDDDDSDASMPFESENETPHARDSCRNNSSQRDPQSQR 77
 71 IVRLVGVR--DWANKNPREBEPDSEFLERFRGPELQTVTHQGD-----DKG 117
 78 EQYLFGAIALFNVNSSNKGDEPKKKKKKKKKSGDKNENKDEKKKKKEKKKK 137
 118 GKDEGGKTK--KAFELFVLDPAGDWYRWLFVLAMPVLYNWCLLVARACPSDLQRNVFV 175
 138 NKEEGKDKKEEKKVWVVDPAANNYNWLFCTILPVMYVNTVIARACFDELQSDYLE 197
 176 VWLVLDYFSDPVYIADLIIRLTQFLEGLLVKPKLKDNDYIHTLOFKLDVASIIPDLD 235
 198 YWIIIFDYLSDIVLLDMFVRTGTGLEQLLVREAKLKYKSNLQPKLDFLSVIPDLD 257
 236 IYFVGHSPVFNRLHFRARMEFFDRTRTSYNIPIRISNLVLYLVIHWNACIY 295
 258 LYFLKGNYPRIRLNRLRIIRMEFFQRTTRTNYPNIPRISNLVYVIHWNACVY 317
 296 YVSKSIGFVDYTWYYPNITDPEGYLAREVIYCYLWSTLTLTITGETPPPVKDEYLFV 355
 318 PSISKAIGFNDTWYYPNDPFGRLARKVYSLYWSLTLTITGETPPPVPRDSEYFV 377

QY 356 IFDFLIGVLIFATIVGNVSMISNNATRAEFOAKIDAVKHVWQFRKYSKDEAKVWKF 415
 DB 378 VDFLIGVLIFATIVGNVSMISNNATRAEFOAKIDAVKHVWQFRKYSKDEAKVWKF 437
 QY 416 DYLWNTKKTVDREVLKMLPAKLRAEIAINVHLSLTKKVRIFQDMWAGLLVELVLKRPQ 475
 DB 438 DYLWNTKKTVDREVLKMLPAKLRAEIAINVHLSLTKKVRIFQDMWAGLLVELVLKRPQ 497
 QY 476 VSPGDYICRKGDKGKMWIIKEGKLVAVDDGVTOYALLSAGSCFGEISILNIKSGKMG 535
 DB 498 VSPGDYICRKGDKGKMWIIKEGKLVAVDDGVTOYALLSAGSCFGEISILNIKSGKMG 557
 QY 536 NRTANIRSLGYSDLFCLSKDLDLMEAVTEAPDAKVKLEERGREILMKGLDENEV-AAS 594
 DB 558 NRTANIKSIGYSDLFCLSKDLDLMEALTEYPPDAKVTWLEEKQILMKDGLDINIANAGS 617
 QY 595 MEVDVQEKLEQLENTNDTLTYTFARLLABYTGAQOKLKORITVLETKM 643
 DB 618 DPRDLEEKVTRMEGSDYLLQTRFARILAEYESMQOKLKORLTKEVERFLK 666
 RESULT 15
 CNGI_MOUSE STANDARD; PRT; 684 AA.
 AC P29974; Q60776;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE cGMP-gated cation channel alpha 1 (CNG channel alpha 1) (CNG-1) (CNGI)
 DE (Cyclic nucleotide-gated channel alpha 1) (Cyclic nucleotide-gated
 DE channel, photoreceptor) (Cyclic-nucleotide-gated cation channel 1)
 DE (Rod photoreceptor cGMP-gated channel alpha subunit).
 GN CNGAL OR CNGC1 OR CNGC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=92210603; PubMed=1372902;
 RA Baehr W., Wasmuth J.J., Hurwitz R.L., Seldin M.F., Howard T.A.,
 RA Altherr M.R., Lee A.K., Pittler S.J.;
 RT "Primary structure and chromosomal localization of human and mouse
 RT rod photoreceptor cGMP-gated cation channel.";
 RL J. Biol. Chem. 267:6257-6262 (1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=95315239; PubMed=7540868;
 RA Karlson K.H., Ciampolillo-Bates F., McCoy D.E., Kizer N.L.,
 RA Stanton B.A.;
 RT "Cloning of a cGMP-gated cation channel from mouse kidney inner
 RT medullary collecting duct.";
 RL Biochim. Biophys. Acta 1236:197-200 (1995).
 CC -!- FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN
 CC COUPLED CASCADE USING CGMP AS SECOND MESSENGER. THIS PROTEIN CAN
 CC BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO AN OPENING OF THE CATION
 CC CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF ROD
 CC PHOTORECEPTORS.
 CC -!- SUBUNIT: Homotetramer or higher oligomer.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Rod cells in the retina and inner medulla of
 CC kidney.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 CC (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
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CC DR EMBL; M84742; AAA37425.1; -;
CC DR EMBL; U19717; AAA85702.1; -;
DR DR EMBL; U19715; AAA85700.1; -;
DR DR EMBL; U19716; AAA85701.1; -;
DR DR MGI; 88436; Cngal.
DR DR InterPro; IPR000595; cNMP binding.
DR DR InterPro; IPR005821; Ion Trans.
DR DR InterPro; IPR001622; K+channel_pore.
DR DR Pfam; PF00027; cNMP_binding; 1.
DR DR Pfam; PF00520; ion_trans; 1.
DR DR SMART; SM00100; cNMP; 1.
DR DR PROSITE; PS00888; cNMP_BINDING_1; 1.
DR DR PROSITE; PS00889; cNMP_BINDING_2; 1.
DR DR PROSITE; PS00442; cNMP_BINDING_3; 1.
KW Ionic channel; ion transport; cNMP-binding; Transmembrane;
KW Multigene family; Vision.
FT DOMAIN 1 156 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 157 177 H1 (POTENTIAL).
FT DOMAIN 178 190 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 191 209 H2 (POTENTIAL).
FT DOMAIN 210 233 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 234 253 H3 (POTENTIAL).
FT DOMAIN 254 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 292 314 H4 (POTENTIAL).
FT DOMAIN 315 366 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 367 386 H5 (POTENTIAL).
FT DOMAIN 387 470 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 471 491 H6 (POTENTIAL).
FT DOMAIN 492 684 CYTOPLASMIC (POTENTIAL).
FT NP BIND 479 601 CGMP (POTENTIAL).
FT BINDING 538 538 CGMP (POTENTIAL).
FT BINDING 553 553 CGMP (POTENTIAL).
FT CARBOHYD 417 417 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 113 114 NK -> I (IN REF. 1).
FT CONFLICT 200 200 D -> N (IN REF. 1).
FT CONFLICT 576 576 A -> V (IN REF. 1).
FT CONFLICT 635 635 R -> C (IN REF. 1).
SQ SEQUENCE 684 AA; 79460 MW; 13E2A405B68CBF CRC64;

Query Match 57.9%; Score 2012.5; DB 1; Length 684;
Best Local Similarity 61.5%; Pred. No. 7.4e-127;
Matches 401; Conservative 87; Mismatches 141; Indels 23; Gaps 6;
QY 21 PPSIKANGKDDHGRGSRQSVAAADDTSPELQRLAEMDTPRG-----RGGFQIRVLV 75
Db 16 PNIVFAIEKEIRRMENACGSFSDDDNGSLSESENESSFFRSNRYKRRGPSQREQHLP 75
QY 76 GV-----IRDWANK-----FREPEPRPSFLERFRGPBLQVTTTHQGD--DKGGK 119
Db 76 GTMALFNVNNSNKKQEPKEXKKKKKKSKADDKNENKDDPEKKKKKEKEKKKKKEK 135
QY 120 DGEKGTKKKFELVDLPAGDWYRWLFVTAMPVLVNWCLLVARACPSDLQRYFVWLV 179
Db 136 TEKKSEEEK- EYVVIDPSGNTYNNWLCITLFPVYNWNTMIARACFDELQSDYLEYWLI 194
QY 180 LDYFSDTVYIADLIIRLTGFLGQLLVKDPKKLRDNYIHTLQPKLDVASIIPDLYFA 239
Db 195 FDVSVVVVYADVFRTRTGILGQLLVKDRMKLIEKYKANLQFKGLVSLVFIPTDLYIK 254
QY 240 VGIHSEVRENRLHFAFMFEFFDRTRTSYPNIFRISNLVLYIIVIIHWNACIYYVIS 299
Db 255 FGWNPYBIRNLLRISRMFEFFORTTETRTNYNIFRISNLVMYVIVIIHWNACVYVIS 314
QY 300 KSTGFGVDTWYVNIPTDPEYGLAREYIYCLYWSTLTLTIGETPPPVKDBEYLVFI 359
Db 315 KATGFGNDTWYVDPVNDPEFRLARKYVSLYWSTLTLTIGETPPPVLDSEYIFVWVDF 374
QY 360 LIGVLIFATVGVNIGSMISNNNATRAEFQAKIDAVKHVMOFRKVKDKMEAKVIKWDYLW 419
Db 375 LIGVLIFATVGVNIGSMISNNNATRAEFQSRVDAIKQYMMNFRNVSKDMEKRVINKW 434

QY 420 TNKKTVDREVLKNIPLAKLRABIAINVHLSTLKKVRIFODWEAGLIVELVLKLPQVFSR 479
Db 435 TNKKTVDREVLRYLPDLKRAEIAINVHLDTLKKVRIFADCEAGLIVELVLKLPQVYSP 494
QY 480 GDYICRKGDIGEMVYIIEGKLAVVADGVTQVALLSAGSCFGEISILNKGSKMGNRRT 539
Db 495 GDYICKKGDIGEMVYIIEGKLAVVADGVTQVALLSAGSCFGEISILNKGSKMGNRRT 554
QY 540 ANIRSLGYSDLECLSKDDLMWVTEAPDAKKVLEERGREILMKMGLLDENEV-AASMEVD 598
Db 555 ANIKSIGYSDLECLSKDDLMWVTEAPDAKKVLEERGREILMKMGLLDENEV-AASMEVD 614
QY 599 VOEKLQLEETNMDTLTYTRFARLLAETGAQOKLQKORITVLETKMKONHEDDY 650
Db 615 LEEKVTRMEGSDVLLQTRFARLLAETGAQOKLQKORITVLETKMKONHEDDY 666

Search completed: May 12, 2004, 11:14:14
Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 12, 2004, 11:11:05 ; Search time 45 Seconds

(without alignments)

4655.646 Million cell updates/sec

Title: US-10-087-217a-8

Perfect score: 3475

Sequence: 1 WMTXSGVYKSPANNHH.....NHEDDYLSDGINTPEPTAAE 664

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mbc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvrius:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3405	98.0	664	11 Q80XH6	Q80XH6 mus musculus
2	2160.5	62.2	631	11 Q8CEV6	Q8CEV6 mus musculus
3	2147.5	61.8	632	11 Q9ER32	Q9ER32 rattus norv
4	2140	61.6	670	11 Q9ER33	Q9ER33 rattus norv
5	2132	61.4	611	11 Q9QW7	Q9QW7 rattus norv
6	2035	58.6	686	6 Q9N04	Q9N04 sus scrofa
7	1927	55.5	637	13 Q80416	Q80416 carassius a
8	1862	53.6	737	13 Q8UV78	Q8UV78 oncorhynch
9	1433	41.2	609	13 Q8JFP0	Q8JFP0 ictalurus p
10	1375	39.6	551	13 Q8JFN9	Q8JFN9 ictalurus p
11	1278.5	36.8	474	4 Q8TV77	Q8TV77 homo sapien
12	1180.5	34.0	900	5 Q97119	Q97119 limulus pol
13	1176	33.8	1218	5 Q9W201	Q9W201 drosophila
14	1128	32.5	252	11 Q9QX26	Q9QX26 rattus norv
15	1068	30.7	1463	5 Q9USE2	Q9USE2 drosophila
16	997	28.7	1324	5 Q8IR35	Q8IR35 drosophila

17	997	28.7	1696	5	Q9VXV8	Q9VXV8 drosophila
18	873.5	25.1	695	5	Q93486	Q93486 caenorhabdi
19	870.5	25.1	1037	5	Q9W2D5	Q9W2D5 drosophila
20	870.5	25.1	1040	5	Q8IH43	Q8IH43 drosophila
21	863.5	24.8	832	5	Q9N4C1	Q9N4C1 caenorhabdi
22	835	24.0	800	5	P90975	P90975 caenorhabdi
23	835	24.0	800	5	O62237	O62237 caenorhabdi
24	831	23.9	644	5	O61827	O61827 caenorhabdi
25	784	22.6	866	11	Q80XL8	Q80XL8 mus musculu
26	782	22.5	809	4	Q9NQW8	Q9NQW8 homo sapien
27	778	22.4	1245	4	O43636	O43636 homo sapien
28	778	22.4	1251	4	Q9UMG2	Q9UMG2 homo sapien
29	773.5	22.3	858	11	O55157	O55157 rattus norv
30	773.5	22.3	1339	11	O35788	O35788 rattus norv
31	770	22.2	938	6	O77658	O77658 bos taurus
32	770	22.2	948	6	O77659	O77659 bos taurus
33	770	22.2	952	6	O77660	O77660 bos taurus
34	758.5	21.8	694	11	Q9UJZ9	Q9UJZ9 mus musculu
35	753	21.7	515	5	Q9S5L0	Q9S5L0 drosophila
36	728	20.9	782	6	Q8WJD7	Q8WJD7 canis famil
37	716.5	20.6	610	4	Q9NRE9	Q9NRE9 homo sapien
38	670	19.3	151	11	P70607	P70607 rattus norv
39	550	15.8	605	5	O7Z205	O7Z205 caenorhabdi
40	516.5	14.9	767	5	O76977	O76977 strongyloce
41	511	14.7	890	4	Q86WJ6	Q86WJ6 mus sapien
42	502	14.4	945	5	Q9Y1J9	Q9Y1J9 drosophila
43	502	14.4	1327	5	Q9V702	Q9V702 drosophila
44	501.5	14.4	678	5	O96777	O96777 heliothis v
45	481	13.8	774	4	Q86WJ5	Q86WJ5 homo sapien

ALIGNMENTS

RESULT 1

ID	Q80XH6	PRELIMINARY;	PRT;	664 AA.
AC	Q80XH6;			
DT	01-JUN-2003 (TtEMBLrel. 24, Created)			
DT	01-JUN-2003 (TtEMBLrel. 24, Last sequence update)			
DT	01-OCT-2003 (TtEMBLrel. 25, Last annotation update)			
DE	Cyclic nucleotide gated channel 4.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUB=Olfactory epithelium;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettewen M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Jones S.J., Marra M.A.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RP	SEQUENCE FROM N.A.			
RC	TISSUB=Olfactory epithelium;			

```
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC048775; AAH48775.1; -.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0002216; F.ion channel activity; IEA.
DR GO; GO:0005267; F.potassium channel activity; IEA.
DR GO; GO:0006811; F.ion transport; IEA.
DR GO; GO:0006813; P.potassium ion transport; IEA.
DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR001622; K+channel_pore.
DR Pfam; PF00027; cNMP_binding_1.
DR Pfam; PF00520; ion_trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; 1.
DR PROSITE; PS00889; cNMP_BINDING_2; 1.
DR PROSITE; PS00042; cNMP_BINDING_3; 1.
SQ SEQUENCE 664 AA; 76192 MW; 34F8DF3B732C0D9C CRC64;

Query Match          98.0%; Score 3405; DB 11; Length 664;
Best Local Similarity 98.2%; Pred. No. 6.5e-244;
Matches 652; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEKSGVKSPPANNHHPPPSIKANGKDDHAGSRPOSVAADDDTSPELQRLAEMDT 60
DB 1 MTEKSGVKSPPANNHHPPPSIKANGKDDHAGSRPOSVAADDDTSPELQRLAEMDT 60
QY 61 PRRGGGFQIRVLGVIRDWANKNFREPRDPSFLERFRGPELQVTTHQGDGKGD 120
DB 61 PRRGGGFQIRVLGVIRDWANKNFREPRDPSFLERFRGPELQVTTHQGDGKGD 120
QY 121 GEGKGTGKKKPELVDPAGDWYRWLFVAMPVLYNWCLLVARACFSDIQRYVWVL 180
DB 121 GEGKGTGKKKPELVDPAGDWYRWLFVAMPVLYNWCLLVARACFSDIQRYVWVL 180
QY 181 DYPGSDTVIADLIIRLTGFEQGLLVKDKPKLRDNYHTLOFKLDVASIIPTDLIYF 240
DB 181 DYPGSDTVIADLIIRLTGFEQGLLVKDKPKLRDNYHTLOFKLDVASIIPTDLIYF 240
QY 241 GIHSPEVRFNRLHFAFMFEFFDRTRTSYPTNFRISNLVLYLVIIHWNACIYYISK 300
DB 241 GIHSPEVRFNRLHFAFMFEFFDRTRTSYPTNFRISNLVLYLVIIHWNACIYYISK 300
QY 301 SIGGVDTWYVNTDPEYGLAREIYICLYWSTLTITIGETPPVKDEEYLFVDFEL 360
DB 301 SIGGVDTWYVNTDPEYGLAREIYICLYWSTLTITIGETPPVKDEEYLFVDFEL 360
QY 361 IGVLI FATVGVNMGSMINMNAATRAEFOAKIDAVKHYMQFRKVKDKMEAKVIKWF 420
DB 361 IGVLI FATVGVNMGSMINMNAATRAEFOAKIDAVKHYMQFRKVKDKMEAKVIKWF 420
QY 421 NKKTVDREVLKNLPDAKRAEIAINVHISTLKKVRIFOQWAGLLVELVVKLPQVSPG 480
DB 421 NKKTVDREVLKNLPDAKRAEIAINVHISTLKKVRIFOQWAGLLVELVVKLPQVSPG 480
QY 481 DYICRKGDI GKEMYIIKESKLAVADDGVTOYALLSAGSCFGEISILNIKSGMGNRTA 540
DB 481 DYICRKGDI GKEMYIIKESKLAVADDGVTOYALLSAGSCFGEISILNIKSGMGNRTA 540
QY 541 NIRSIGSYDLFCLSKDDLMEAATEAPDAKKVLEERGREILMKWGLLDENEVAASVEDVQ 600
DB 541 NIRSIGSYDLFCLSKDDLMEAATEYFDPAKKVLEERGREILMKWGLLDENEVAASVEDVQ 600
QY 601 EKLEQETNMDTLYTRFARLLAEYGAQOKLQRTITVETQKQNHEDDYLSDGINTPEP 660
DB 601 EKLEQETNMETLYTRFARLLAEYGAQOKLQRTITVETQKQNHEDDYLSDGINTPEP 660
QY 661 TAAE 664
DB 661 AVAE 664

Query Match          62.2%; Score 2160.5; DB 11; Length 631;
Best Local Similarity 67.0%; Pred. No. 1.3e-151;
Matches 412; Conservative 85; Mismatches 93; Indels 25; Gaps 5;

QY 57 EMDPRRGRGGFQIRVLGVIRDWANKNFREPRDPSFLERFRGPELQVTTHQ---- 112
DB 24 DLDDHVENGLG---RVSRLLIISIRAWASHLHDEQCTDPSFLDRFHGSELKEVSRESNAQ 80
QY 113 ---GDGKGGKDEGEGKGTGKKKPELVDPAGDWYRWLFVAMPVLYNWCLLVARACFSD 169
DB 81 PNPGEQKPPDGGEG---RKEEPIVDPSSNIYYRWLTALPVPFYNWCLLVCRCACFDEL 136
QY 170 QRYFVFWWLVLDYSDTVIADLIIRLTGFEQGLLVKDKPKLRDNYHTLOFKLDVAS 229
DB 137 QSEHLTLWLVLDYSDTVIADLIIRLTGFEQGLLVKDKPKLRDNYHTLOFKLDVAS 196

Query Match          62.2%; Score 2160.5; DB 11; Length 631;
Best Local Similarity 67.0%; Pred. No. 1.3e-151;
Matches 412; Conservative 85; Mismatches 93; Indels 25; Gaps 5;

QY 57 EMDPRRGRGGFQIRVLGVIRDWANKNFREPRDPSFLERFRGPELQVTTHQ---- 112
DB 24 DLDDHVENGLG---RVSRLLIISIRAWASHLHDEQCTDPSFLDRFHGSELKEVSRESNAQ 80
QY 113 ---GDGKGGKDEGEGKGTGKKKPELVDPAGDWYRWLFVAMPVLYNWCLLVARACFSD 169
DB 81 PNPGEQKPPDGGEG---RKEEPIVDPSSNIYYRWLTALPVPFYNWCLLVCRCACFDEL 136
QY 170 QRYFVFWWLVLDYSDTVIADLIIRLTGFEQGLLVKDKPKLRDNYHTLOFKLDVAS 229
DB 137 QSEHLTLWLVLDYSDTVIADLIIRLTGFEQGLLVKDKPKLRDNYHTLOFKLDVAS 196
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QY 230 LIPTDLIYFAVGIHSPVRFNRLHFAFMFFDFDTETRTSYPNLFRISNLVLYLIIH 289
DB 197 LIPTDLVILKLGNYPELDFNRLHFAFMFFDFDTETRTSYPNVFRIGNLVLYLIIH 256
QY 290 WNACTIYVLSKIGFQDVTWVYVNTDPEYGLAREYIYCLYWSLTLTTTIGETPPVKD 349
DB 257 WNACTIYFALSIGFQDVTWVYVNTDPEYGLAREYIYCLYWSLTLTTTIGETPPVKD 316
QY 350 EBYLFIYFDFLIGLVLFATVGNVSGMISNMNATRAEFOAKIDAVKHYNQFRKVSQDMEA 409
DB 317 EBYLFIYFDFLIGLVLFATVGNVSGMISNMNAPRVEFOAKIDSVKQYMQFRKVTNDLET 376
QY 410 KVIKPFYDNLWNTKVTDEVEVLKNLPAKRAETAINVHLSTLKKVIFODWEAGLLVELV 469
DB 377 RVIRPFYDLWANKTVDDEVEVLKNLPAKRAETAINVHLSTLKKVIFODWEAGLLVELV 436
QY 470 LKLRPOVSPGDIYCKRGDIKEMYYIIEKGLAVVADDGVTQVLLSDGSGYFGEISILNI 529
DB 437 LKLRPVTSPGDIYCKRGDIKEMYYIIEKGLAVVADDGVTQVLLSDGSGYFGEISILNI 496
QY 530 KSGKGNRRNTANRSIGYSDFLCLSKODLMEAVTEAPDAKVLBERGRILMKOGLLDEN 589
DB 497 KSGKGNRRNTANRSIGYSDFLCLSKODLMEALTEYPDARALEEKGROQLMKONLIDED 556
QY 590 EVAASMEV-DVQEKLEQLENTMDTLVTRFARLLAEYTGQOKLORITVLETKM----- 642
DB 557 LVAARVTRDVEKVEYLESSLDLQTRFARLLAEYSQMKLQKRLTRLESQNRRCGG 616
QY 643 ----KQHEDDYLS 653
DB 617 FSPDENSEDASKTD 631

RESULT 3
Q9ER32 ID Q9ER32 PRELIMINARY; PRT; 632 AA.
AC Q9ER32;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Cyclic nucleotide-gated channel 2a.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=20442421; PubMed=10984544;
RA Meyer M.R., Angele A., Kremer E., Kaupp U.B., Mueller F.;
RT "A cGMP-signalling pathway in a subset of olfactory sensory neurons.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:10595-10600(2000).
DR EMBL; AJ272429; CAC09431.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potaassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potaassium ion transport; IEA.
DR InterPro; IPR000595; cNMP_binding.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00027; cNMP_binding_1.
DR Pfam; PF00520; ion_trans_1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; 1.
DR PROSITE; PS00889; cNMP_BINDING_2; 1.
DR PROSITE; PS00890; cNMP_BINDING_3; 1.
DR KW Ionic channel; Transmembrane.
SQ SEQUENCE 632 AA; 72536 MW; 2A48AAECDD600D37 CRC64;

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Query Match 61.8%; Score 2147.5; DB 11; Length 632;
 Best Local Similarity 64.5%; Pred. No. 1.2e-150;

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Matches 407; Conservative 94; Mismatches 103; Indels 27; Gaps 5;
QY 39 PQSVAADDDTSPQLQLAEMDTPRGRGGRFIVELGVIRDWANKNFRFEEPRDPSUE 98
DB 13 PQUSVKDAARDLDDQV-----ENGLGRVSRFIISIRAWAARHLHHEPTDPSFLD 63
QY 99 RPRGPELOTVITHQDDKGGKQGE-----GKGTKKKFFELVLDPADGMYRWLFVIAMPV 153
DB 64 RPHGAELKEVSSQERNAQFPGQEPPEGGKGRKK-DPIVVDPSNIIYRWLTALP 121
QY 154 LYNWCLLVARCFSDLQRNYFVWVLDYFSTVTIADLIIRLTGTFLEOGLLVKPKL 213
DB 122 FYNWCLLVCRAFCSLQSEHLTLWLVDYSDALYVDMVLRARTGFLEQGLMVRDTK 181
QY 214 RNYTHITQFKLDVASIITPTDLIYFAVGHSPEVFRNLLHFAFMFFDFDTETRTSYN 273
DB 182 WKHYTKLHFKLDIISLPTDLAYLKLGNVYELAFNRLRFSRLEFFDRTETRTSYN 241
QY 274 IFRISNLVLYLIIHWNACIYVYVSKSIGFQDVTWVYVNTDPEYGLAREYIYCLYWS 333
DB 242 VFRIGNLVLYLIIHWNACIYFAISKFIFGFGTDSWVYENTSKPEYGRLSRYIYSLYWS 301
QY 334 TLTLTTIGETPPVKDDEEVLVIFDFGLGLVLFATVGNVSGMISNMNATRAEFOAKIDA 393
DB 302 TLTLTTIGETPPVKDDEEVLVIFDFGLGLVLFATVGNVSGMISNMNATRAEFOAKIDA 361
QY 394 VKHYMQFRKVSQKMEAKVWKFDYILWNTKKTVDREVLKXNLPKLAETAINVHLSTLKK 453
DB 362 IKQYMQFRKVTXDLFTRVIRWFDYLVWANKTVDREVLKXNLPKLAETAINVHLSTLKK 421
QY 454 VRIFQDWEAGLLVELVILKURPOVSPGDIYCKRGDIKEMYYIIEKGLAVVADDGVTQYA 513
DB 422 VRIFQDWEAGLLVELVILKURPAVSPGDIYCKRGDIKEMYYIIEKGLAVVADDGVTQYV 481
QY 514 LLSAGSCFGEISILNIKSGMGNRRNTANRSIGYSDFLCLSKODLMEAVTEAPDAKVL 573
DB 482 VLSDGSGYFGEISILNIKSGMGNRRNTANRSIGYSDFLCLSKODLMEALTEYPDARALE 541
QY 574 ERGREILMKGLIDENEVAASMEV-DVQEKLEQLENTMDTLVTRFARLLAEYTGQOKLK 632
DB 542 EKGRQILMKGLIDDLVTRADARNIEKVEYLESSLDLQTRFARLLAEYSQMKLK 601
QY 633 QRTVILETKM-----KQHEDDYLS 653
DB 602 QRLSQLESQMTGRGHGFSFDENSEDASKAD 632

RESULT 4
Q9ER33 ID Q9ER33 PRELIMINARY; PRT; 670 AA.
AC Q9ER33;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Cyclic nucleotide-gated channel 2b.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory epithelium;
RX MEDLINE=20442421; PubMed=10984544;
RA Meyer M.R., Angele A., Kremer E., Kaupp U.B., Mueller F.;
RT "A cGMP-signalling pathway in a subset of olfactory sensory neurons.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:10595-10600(2000).
DR EMBL; AJ272428; CAC09430.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potaassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potaassium ion transport; IEA.
DR InterPro; IPR000595; cNMP_binding.

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QY 451 LKVRIFQDWEAGLLVVLKLPQVSPGDYICRKGDIGKEMYYIIKEGKLAVVADGVT 510
Db 817 LKRVFQNTAEGLCELVLRLPVLSPGDYICRKEVGKEMYIYNRGLQVAVDNGKT 876
QY 511 QYALLSAGSGEISILNKGSKMGNRTNIRISLGYSDLFCLSKDLMBAVTEADPAK 570
Db 877 VMASLKAGSYFGEISILNM--GTAGNRTASVRSVGYSDLFVLSKKMDMDVLKEYPAARV 934
QY 571 VLE 573
Db 935 RLE 937

RESULT 14
Q9QX26 PRELIMINARY; PRT; 252 AA.
AC Q9QX26;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclic nucleotide-gated cation channel (Fragment).
GN CNG3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Qiu W., Guggino S.E.;
RT "Cyclic nucleotide-gated cation channel (CNG3) expression in rat
kidney.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031943; AAB87065.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006913; P:potassium ion transport; IEA.
DR InterPro; IPR000595; cNMP binding.
DR Pfam; PF00027; cNMP binding; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP BINDING_1; 1.
DR PROSITE; PS00889; cNMP BINDING_2; 1.
DR PROSITE; PSS0042; cNMP BINDING_3; 1.
FT NON TER 1 252
FT NON TER 252 252
SQ SEQUENCE 252 AA; 28677 MW; C59A1CF7654AA894 CRC64;

Query Match 32.5%; Score 1128; DB 11; Length 252;
Best Local Similarity 85.3%; Pred. No. 1.4e-75;
Matches 214; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

QY 317 PEYGLAREYICLYWSLTTLTTIGETPPPVKDEYLFVDFLIGLVLFATIVGVN 376
Db 2 PEYGLSKYISLYWSLTTLTTIGETPPPVKDEYLFVDFLIGLVLFATIVGVN 61
QY 377 ISNNATRAEFQAKIDAVKHYMQPRKYSKMEAKVIKWFYDLWNTKKTVDREV 436
Db 62 ISNNASRAEFQAKIDSIKQTMQPRKVTQKLETRVIRWFDYLVANRKTVDKE 121
QY 437 KLRAEIINVHLSLTKVRIQDWEAGLLVVLKLPQVSPGDYICRKGDIGKEM 496
Db 122 KLRAEIINVHLSLTKVRIQDWEAGLLVVLKLPQVSPGDYICRKGDIGKEM 181
QY 497 KEGKLAVVADGVTQYALLSAGSGEISILNKGSKMGNRTNIRISLGYSDLF 556
Db 182 KEGKLAVVADGVTQYVVLSDGSYFGEISILNKGSKMGNRTNIRISLGYSD 241
QY 557 DLMBAVTEAD 567
Db 242 DLMETLTYPE 252

RESULT 15

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Q9U5E2 PRELIMINARY; PRT; 1463 AA.
AC Q9U5E2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CNG channel-like.
GN CNGL OR CG9176.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Miyazu M., Tanimura T.;
RT "A putative CNG-channel of Drosophila melanogaster.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB030577; BAA89278.1; -.
DR FlyBase; FBgn0029090; cngl.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006911; P:ion transport; IEA.
DR GO; GO:0006913; P:potassium ion transport; IEA.
DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR005821; Ion Trans.
DR InterPro; IPR001622; K+channel_pore.
DR Pfam; PF00027; cNMP binding; 1.
DR Pfam; PF00520; ion_trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP BINDING_1; 1.
DR PROSITE; PS00889; cNMP BINDING_2; 1.
DR PROSITE; PS00042; cNMP BINDING_3; 1.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 1463 AA; 159935 MW; D902602E351D42C2 CRC64;

Query Match 30.7%; Score 1068; DB 5; Length 1463;
Best Local Similarity 35.6%; Pred. No. 5.2e-70;
Matches 234; Conservative 136; Mismatches 206; Indels 82; Gaps 15;

QY 80 DWANKNFR-----EEEP---RPDSFLERF---RQPELQTVTHQDDKGGK 119
Db 39 DWTRSNQRWMLRTTVQISSAIQKPKLPKREDSFLKRFSTRQIPETQETVEDT 98
QY 120 DGEKGKTKKKFELF-----VLDPAQDWYRVLVPIAMPVLYNWLCLVARCF 174
Db 99 DVD-KSVKRRRVLOKRRSVNPDENFYFWLMLTVCLVNLWTLIVRQSPFELQ 157
QY 175 VVWLVDYFSDTVYIADLIIRLTATGFLQGLLVKDPKLRDNYHTLQFKLDVASI 234
Db 158 TFWLICDSMTDVVFIIDIIIVQLATGYLEQGLMYDDRKACHYVHSRDETFD 217
QY 235 LIYPAGVGHSPVRENRLLHFARMEFEEDTERTSYPNIFRISNLVLYLVIH 294
Db 218 LLQLKMGTH-PLKURTRFPKVRYSRVFYIVESRTVWPNLWVNLHILLIAH 276
QY 295 YVVISKSGIGVDVTWYYPNIITDEPYGLAREYICLYWSLTTLTTIGETPP 354
Db 277 YFLSEAGFGQD-WVYP-YRPGDYPLTRKYLGLSWSLTLTTIGDLPETNAE 334
QY 355 VIFDFLIGLVLFATIVGVNVSMSNNATRAEFQAKIDAVKHYMQPRKYSKME 414
Db 335 TIYSYLIGVFIFATIVGVGNVTNRNANRLEFERLLDGAKTVMRHHKVP 394
QY 415 FDYLVNKKTV---DEREVLKNI-PAKLRAEIINVHLSLTKVRIQDWEAG 471
Db 395 YDYSWSRGRIQGGGDINTALGLLPDKLTALAUVNLVLKVKVTFIQECQ 454
QY 472 LRQVTFSPGDYICRKGDIGKEMYYIIKEGKLAVVADGVTQYALLSAGSG 531
Db 455 MKAYITPQDSICRKGVEAREMEFIADGILEVLSETKV-LTTMKAGDFGEIG 513

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QY 532 SKMGNRTANIRSGYSDLFCLSKDDLMEAVTEAPDAKKVLEERGRELMMKGLLDENEV 591
Db 514 L---NKRTADVRSVGYSELSFSLREDVLAAMKDYFDAQEIIQTLGRKELMEVRCVNKKYA 570
QY 592 AASMEVDV-----QEKLEQLETNMDTLYTREA-RLLAEYTGAAQOKLKQRI 635
Db 571 KAQSDKEAAAYAAAHPHHHQSHHQVHQSDSENSASKKIVDKLKHDKGFRNVLKXSR 630
QY 636 T-----VLETKMKQNHEDDYLSDGI-----NTPEPTA 663
Db 631 TSRKSDSELEMOPLHNTSPRGSKILLKRWRSRDEKDDASAAKDELHDKTSPFIGA 688
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Search completed: May 12, 2004, 11:15:12
Job time : 47 secs